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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

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US-10-10-10-77-1
US-10-110-777-1
US-10-110-777-1
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US-10-172-118-442
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RESULT 2 US-60-391-781-685 ; Sequence 685, Application US/60391781

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Query Match
Best Local Similarity
Matches 142; Conserv

Conservative

12.6%;

Score 125.8; DB 7; Pred. No. 6.6e-20; 0; Mismatches 27;

Length 2554; Indels

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Gaps

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880 gaggacttaaaatccttgatcgatagagcacatgagcttggtttgcttgttcttatggat 658 gaggacttaaaatccttgatcgatagagcacatgagcttggtttgcttgttcttatggat 820 gcgagctttgggtaccatgttactaatttttttgcaccaagtagccgttttggaactcca 879 598 gcttgttccaggtaccatgttactaatttttttgcaccaagtagccgttttggaactcca

RESULT 1 US-10-162-948 Sequence 1, GENERAL INF APPLICANT: FILE REFER CURRENT APPL PRIOR APPL PRIOR APPL PRIOR APPL PRIOR FILL NUMBER OF SOFTWARE: SEQ ID NO 1 LEGITH: 2 TYPE: DNA ORGANISM: FEATURE: NAME/EYF: NAME/EYF LOCATION: US-10-162-948	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
42K:XZ :TFDTAE HHHHHZ14	0.4 4 222222 0.0 4 9.0 9.0 8.0 0.0 6.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9
1. Application US/ 1. Application US/ 1. Application US/ 1. Application US/ 1. Napomarion: Jay-in 1. Janes, Jay-in 1. Janes, Jay-in 1. Sun, Chianxin 1. Sun, Chuanxin 1. Invention Transg 1. Invention UMBER: 1. Patentin Ver. 2. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	50 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6
1, Application US/101629 1, Application US/101629 1NFORMATION: TT: Jane, Jay-lin TT: Sun, Christer TT: Sun, Chuanxin TI: On UNANGENIC Corneration: TRANSGENIC TRENCE: 480927.9081 TING DATE: 2002-06-07 PELING DATE: 2002-06-07 PELING DATE: 2001-06-04 THE SEQ ID NOS: 12 THING DATE: 2001-06-04 THE SEQ ID NOS: 12 THE SEQ ID NOS	2638 2096 338 2502 2250 2250 1497 6352 2187 6352 2187 6352 576 576 576 576 576 576
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948 CORN PLANTS HAVING SEEDS CHARACTERISTICS AND METI CORN PLANTS 17 7,649	US-60-360-039-27656 US-10-213-073-149 US-10-216-364-138 US-10-219-999-2845 US-60-360-039-43535 US-60-360-039-47275 US-60-377-240-3533 US-60-377-240-3533 US-10-198-846-1482 US-10-198-846-1482 US-10-198-946-1482 US-10-182-995-9523 US-10-182-997-8111 US-10-182-997-8111 US-10-182-997-8111 US-10-182-997-8111 US-10-203-135-12110 US-10-203-135-12110 US-10-203-139-12184 ALLIGNMENTS
WITH MODIFIED HOD OF MAKING THE	Sequence 27656, A Sequence 149, App Sequence 2845, Ap Sequence 43535, A Sequence 24, Appl Sequence 47275, A Sequence 12520, Ap Sequence 12520, Ap Sequence 12520, Ap Sequence 12520, Ap Sequence 12611, Ap Sequence 12611, Ap Sequence 12611, Ap Sequence 12110, Ap Sequence 12184, A

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; ORGANISM: Zea mays
US-60-391-781-685
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                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 201; Conserv
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PRIOR ETLING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 3034
SEQ ID NO 709
LENGTH: 2919
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SEQ ID NO 685
LENGTH: 3144
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Pred. No. 3.6e-15;
0; Mismatches 27
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; GENERAL INFORMATION:
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Best Local Similarity 58.2%;
Matches 178; Conservative
APPLICANT: Pearlstein, Richard W.
APPLICANT: Broglie, Karen E.
APPLICANT: Hines, Christopher F.
TITLE OF INVENTION: Maize Starch Containing Elevated Amounts of Actual Amylose FILE REFERENCE: BB1510PRV1
CURRENT APPLICATION NUMBER: US/60/381,534
CURRENT FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 6
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APPLICANT: Hines, Christopher F.

TITLE OF INVENTION: Maize Starch Containing Elevated Amounts of Actual Amylose FILE REFERENCE: BB1510PRV
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CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 6
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LOCATION: (1)..(2443)
OTHER INFORMATION: SBEII modified region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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Pred. No. 1.5e-11;
0; Mismatches 126;
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SOFTWARE: PatentIn version SEQ ID NO 1

LENGTH:

2443

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US-10-056-454A-17
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; LOCATION: (1)..(2443)
; OTHER INFORMATION: SBEII modified region
US-60-381-534-1
;
US-10-056-454A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 58.2
Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/10056454A GENERAL INFORMATION:
                                                                                                   FILING DATE: 25-Jun-2002 INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: National Starch and Chemical Investment TITLE OF INVENTION: Improvements in or Relating to NUMBER OF SEQUENCES: 20
                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atggaa 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atgcaa 430
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                                      LENGTH: 2529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                     CITY: Newcastle
STATE: Delaware
                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                 STREET: 1000 Uniqema
                              TOPOLOGY: linear
                                                                                                                                APPLICATION NUMBER: US/10/056,454A
               DESCRIPTION:
                                                                                                                                                                                                                                                        United States
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               17:
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                                                                                   RESULT 8
US-10-056-454A-19
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US-10-056-454A-16
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Sequence 19, Application US/10056454A
GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Best Local
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APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2576 base pairs
                                                                                                                                                                                                                   1165
                                                                                                                                                                                                                                                                                     1105 GCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCC 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1220 ATTGTTCACAGCCATGCATCAAATAATACTTT 1251
                                                                                                                                                     1225 ATTGTTCACAGCCATGCATCAAATAATACTTT 1256
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                                                                                                                                                                      718 attgttcataggtaattagtccaatttaattt 749
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APPLICATION DATA:

APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch
1000 Uniqema Blvd.
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                      gaggacttaaaatccttgatcgatagagcacatgagcttggtttgcttgttcttatggat 717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
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73.7%;
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O; Mismatches
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Pred. No.
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5.5e-11;
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SEQUENCE DESCRIPTION: SEQ ID NO: 12: 05-10-056-454A-12
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US-10-056-454A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/10056454A
GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 112; Conserv
                                                                                            INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3003 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIAL PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION NOMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 2578 base pairs
TYPE: nucleic acid
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                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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ADDRESSEE: National Starch and Chemical Investment Holding Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGTTCACAGCCATGCATCAAATAATACTTT 1258
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CITY: Newcastle
STATE: Delaware
                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States of America ZIP: 19720
                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Delaware
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O; Mismatches
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NAME/KEY: CDS
LOCATION: 145..2790
SEQUENCE DESCRIPTION: SEQ
US-10-056-454A-14
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US-10-056-454A-14
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                                                                                                                                                                                  8.8%;
Best Local Similarity 73.7%;
Matches 112; Conservative
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Best Local Similarity
Matches 112; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 25-Jun-2002 INFORMATION FOR SEQ ID NO: 14:
                                                                                                                            1450
                                                               1390 GACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAAGGAATTGTTGTTCTCATGGAC 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1449 ATTGTTCACAGCCATGCATCAAATAATACTTT 1480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: National Starch and Chemical Investment Holding Corporation of INVENTION: Improvements in or Relating to Plant Starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ATTGTTCACAGCCATGCATCAAATAATACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Newcastle
                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3033 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                                                                linear
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73.7%;
                                                                                                                                                                                                                                                                                                                                                                            single
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                                                                                                                                                                                              Score 88; DB 7; Length 3033; 
Pred. No. 5.7e-11; 
0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                ID NO: 14:
1481
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5.7e-11;
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US-10-056-454A-18

; Sequence 18, Application US/10056454A

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RESULT 12
US-10-056-454A-13
Sequence 13, Application US/10056454A
GENERAL INFORMATION:
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APPLICANT: National Starch and Chemical Investment
TITLE OF INVENTION: Improvements in or Relating to
                                APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2975 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/056,454A FILING DATE: 25-Jun-2002 INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1533 ATTGTTCACAGCCATGCATCAAATAATACTTT 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1413 GCTAGTTTTGGTTATCATGTCACAAATTTTTTTGCACCAAGCAGCCGTTTTGGAACGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  718 attgttcataggtaattagtccaatttaattt 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          658 gaggacttaaaatccttgatcgatagagcacatgagcttggtttgcttgttcttatggat 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  598 gcttgttccaggtaccatgttactaatttttttgcaccaagtagccgttttggaactcca 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 3231 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSEE: MATIONAL Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
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COMPUTER READABLE FORM:
                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: National Starch and Chemical Investment TITLE OF INVENTION: Improvements in or Relating to
                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTGTTGTTCTCATGGAC
                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                COUNTRY: United States of America ZIP: 19720
                                                                                                                                                                                                                                                               CITY: Newcastle
STATE: Delaware
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COMPUTER: IBM PC COMPOSITION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Newcastle
STATE: Delaware
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                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No. 5.8e-11;
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                                                                                                                                           #1.30
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tarch Composition
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                                  RESULT 14
US-10-110-777-1
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Sequence 1, Application US/10110777 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              Matches
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Best Local :
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LENGTH: 2324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (3)..(2027)
                                                                                                     570 ctgatggatgttgtccatag
                                                                                                                       709 cttatggatattgttcatag 728
                                                                                                                                                                                                                                                                                                              Local Similarity 69.3 tes 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Edgerton, Michael D
Hinkle, Gregory J.
Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu, Jingdong
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69.3%;
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                                                                                                     589
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Sequence 16451, Application US/10219999
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TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/312,544 PRIOR FILING DATE: 2001-08-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 658 gaggacttaaaatccttgatcgatagagcacatgagcttggtttgcttgttcttatggat 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            598 gcttgttccaggtaccatgttactaatttttttgcaccaagtagccgttttggaactcca 657
510 ggcacaccagaggacctcaaatatcttgttgataaggcacacagtttgggtttgcgagtt
                       649 ggaactccagaggacttaaaatccttgatcgatagagcacatgagcttggtttgcttgtt 708
                                                                                        450 tcgtactatgcttctttcgggtaccatgtgacaaatttctttgcggttagcagcagatca 509
                                                                                                                718 attgttcataggtaattagtccaatttaattt 749
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0; Mis
                                                                                                                                                                                                      Score 71.2; DB
Pred. No. 5e-07;
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Pred. No. 3.2e-10;
0; Mismatches 42
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                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                      43;
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                                                                                                                                                                                                                            Length 2324;
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APPLICANT:

National Research Council of Canada

Baga, Monica

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                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_000158
; DATABASE ENTRY DATE: 2001-06-18
PCT-US02-18947-442
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
PCT-US02-18947-442
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; TYPE: DNA
; ORGANIZM: Triticum aestivum
US-10-110-777-1
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TITLE OF INVENTION: Starch Branching Enzymes
FILE REFERENCE: 45187
CURRENT APPLICATION NUMBER: US/10/110,777
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: PCT/CA00/01276
PRIOR FILING DATE: 2000-10-27
PRIOR PPLICATION NUMBER: US60/162,144
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEO ID NOS: 2
                                                                                                                                                                                                                                                                                                                       Sequence 442, Application PC/TUS0218947
GENERAL INFORMATION:
APPLICANT: Rosetta Inpharmatics
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-228
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Best Local Similarity
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LENGTH: 2913
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PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
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Search completed: September 12, Job time: 11199 sec 2002, 09:13:22

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September 12, 2002, 07:30:52; Search time 5258.2 Seconds (without alignments) 4114.507 Million cell updates/sec
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SUMMARIES

Result

Query

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APPLICANT: KALEEN, ZHONGYILI

APPLICANT: MORELL, MATTHEW
APPLICANT: RAHMAN, SADEQUR
APPLICANT: RAHMAN, SADEQUR

TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN
FILE REFERENCE: 054270/0126
CURRENT APPLICATION NUMBER: US/09/508,377
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: AU PP 2509
PRIOR APPLICATION NUMBER: AU PP 2509
PRIOR APPLICATION NUMBER: PCT/AU98/00743
PRIOR APPLICATION NUMBER: PCT/AU98/00743
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: AU PP 9108
PRIOR FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                           ; SEQ ID NO 10
; LENGTH: 11463
; TYPE: DNA
; ORGANISM: Triticum t
US-09-508-377-10
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Sequence 10, App.
GENERAL INFORMAT
APPLICANT: KAL
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FILE REFERENCE
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US-60-191-687-39923
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Pred. No. 2.3e-282;
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; Sequence 5263, Application US/09887272A
APPLICANT: Quan, Sheng
APPLICANT: Quan, Sheng
APPLICANT: Chang, Hur-Song
APPLICANT: Whitham, Steve
APPLICANT: Whitham, Steve
APPLICANT: Goff, Steve
APPLICANT: Glazebrook, Jane
APPLICANT: Glazebrook, Jane
APPLICANT: Katagiri, Fumiaki
APPLICANT: Xie, Zhiyi
APPLICANT: Tao, Yi
APPLICANT: Tao, Yi
APPLICANT: Cooper, Bret
TITLE OF INVENTION: PLANT GENES INVOLVED
APPLICANT: 1360.003US2
CURRENT APPLICATION NUMBER: US/09/887,277
CURRENT APPLICATION NUMBER: 60/213,634
PRIOR APPLICATION NUMBER: 60/214,926
PRIOR APPLICATION NUMBER: 60/214,926
PRIOR APPLICATION NUMBER: 60/261,320
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/261,320
PRIOR FILING DATE: 2000-06-12
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GENERAL INFORMATI
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PRIOR APPLICATION NUMBER: 60/264,353
PRIOR FILLING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/273,879
PRIOR FILLING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 09/887,271
PRIOR FILLING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 6813
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 5263
LENGTH: 2000
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US-09-887-272A-5263
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                                                                                                                                  YKYMRMYMYKGWMYMMYYSAYSSMMTWYYYYAKYWKYWYKRRGTMSWYGKSYKKKYCTWW
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                                             SWSRWCRSYSWYKMYKKMWKKSYYMSYGWARSSGTWSRSAAKRTYKGYSTSRRAKMMRAC
                                                                      acaatcagacactcaccaactgcttttgtctgggacacaataaatgtttttgtaaacaaa
                                                                                                       CYMKCMRCYRWRKMMRKKTKYSKRCYCWRYATCYWCCCYRKRGWYSRRSMMRTAGKWKMR
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APPLICANT: Hunter, John J.

APPLICANT: Shyjan, Andrew W.

APPLICANT: Shyjan, NOVEL NUCLEIC ACID MOLECULES ANI

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 1600.2084-001

CURRENT APPLICATION NUMBER: US/09/824,628

CURRENT FILING DATE: 2001-04-02

PRIOR APPLICATION NUMBER: US 60/193,423

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 9973

SOFTWARE: FastSEQ for Windows Version 4.0

AND

USES

US-09-824-628-1988

Sequence 1988, Applic GENERAL INFORMATION:

Application US/09824628

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; LOCATION: (1)...(457)
; OTHER INFORMATION: n = A,T,C
US-09-824-556-1988
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RESULT
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GENERAL INFORMATION:
APPLICANT: Hunter, John J.
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 9973
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1988
LENGTH: 457
                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                Matches
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CURRENT APPLICATION NUMBER: US/09/824,556
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: US 60/193,423
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo
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                                                                     YWYMSYMRYMMKCMCSRSCSSWMSCAYCSTSSTSRWMSMYYAAKMGMCGSSGMYRMSKSC
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CURRENT APPLICATION NUMBER: US/09/698,014
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/162,363
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 6098
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
SEQ ID NO 36
TYPE: DNA
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; NAME/KEY: misc_feature
; LOCATION: (1)...(623)
; OTHER INFORMATION: n = A,T,C or
US-09-698-014-36
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; LOCATION: (1)...(457)
; OTHER INFORMATION: n = A,T,C
US-09-824-628-1988
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GENERAL INFORMATION:

APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Kingsbury, Gillian A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2014-001
                                                                                                                                                                                                                                     Matches 102;
                                                                                                                                                                                                                                                   Query Match 4.18;
Best Local Similarity 50.2%;
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Best Local S
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LENGTH: 457
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ORGANISM: Homo
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                                                                    476
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                                                                                                434 gttaacagaactttttcaacaaagcaaggtcaatatgcagaaaatgctcccagaaattga
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Local Similarity 43.48;
hes 75; Conservation
                                                 tcaaaccatgcaccgacgagtccatgcgaggtggaaacgaaggaactgaaaatcaacatcc 535
                                                                                                                   caaacacatgcattttcaaacaaggaaaattaattctcaaaccaccatgacatgcaattc 475
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CURRENT APPLICATION NUMBER: US/09/534,859
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 1127
SEQ ID NO 818
LENGTH: 79976
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-534-859-818
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Best Local Similarity
Matches 120; Conserv
                                  NUMBER OF SEQ ID NOS: 1582
SEQ ID NO 818
LENGTH: 79976
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                                                                                                                                                                      APPLICANT: Rounsley, Steven D.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Plant Polymorphic Markers and
FILE REFERENCE: 38-10(15493)D
CURRENT APPLICATION NUMBER: US/09/803,736
CURRENT FILING DATE: 2001-03-12
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                                                                                                 PRIOR APPLICATION NUMBER: identified by PRIOR FILING DATE: 2000-10-20
                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/534,859 PRIOR FILING DATE: 2000-03-29
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ORGANISM: Arabidopsis thaliana
                      TYPE:
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Levin, Irena M.
                                                                                                                                                                                                                                                                                               Norris, Susan R.
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Pred. No. 14;
0; Mismatches 131;
                                                                                                                    Attorney Docket number 04983.0206CPUS01
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us-09-803-736-818

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Best Local Similarity
                                                                                                                                                                                                                                                               Matches
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SOFTWARE: FastSEQ for Windows Version
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CURRENT FILING DATE: 2001-07-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                             507 tggaaacgaagaactgaaaatcaacatcccagttgtcgagtcgagaagaggatgacactg
     761
                                                                  701
                                                                                                                             641 armgnttywsnwsnytncaygcngtnytntayttywsnccngayttyatgwsnytnggnt 700
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Similarity 25.4%; Pred. No. 1.
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Pred. No. 14;
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; ORGANISM: Arabidopsis thaliana
US-09-692-412-73
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LENGTH: 82356
TYPE: DNA
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CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS:
120 TENERS 1 NO 73
                                                                       Query Match 4.1
Best Local Similarity 52.7
Matches 88; Conservative
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Best Local Similarity
Matches 88; Conserv
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LENGTH: 82356
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APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Plant Polymorphic Markers
FILE REFERENCE: 38-10(15493)D
CURRENT APPLICATION NUMBER: US/09/803,736
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 09/534,859
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: identified by Attorney Docket number 04983.0206CPUS01 38 PRIOR FILING DATE: 2000-10-20 NUMBER OF SEQ ID NOS: 1582
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43442 TCTCAAACTAGCTATAAGTTTTTTTTAATAAAAAACCGAATCAAAACTCAAATCGA 43383
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                   368 tctggaaattcatagctcacactttttttttaatggaagcaagagttggcaaacacatgca 427
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Norris, Susan R.
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                                                                         Score 40.6; D
Pred. No. 25;
0; Mismatches
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RESULT 12
US-09-815-264-74236/c
Sequence 74236, Application US/09815264
; GENERAL INFORMATION:
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APPLICANT: Wu, Wei
TITLE OF INVENTION: Genomic Plant Sequences An
FILE REFERENCE: 38-21(51237)G
CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/702,134
PRIOR FILING DATE: 2000-10-31
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LENGTH: 2085
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Best Local (
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Local Similarity 50.5%;
les 98; Conserva+:...
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Kovalic, David K.
Liu, Jingdong
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McIninch, James
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RESULT 14
US-09-702-134-9663
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; ORGANISM: Oryza
US-09-815-264-74236
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Best Local S
Matches 98
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SEQ ID NO 1096
LENGTH: 2140
TYPE: DNA
ORGANISM: Oryza sativa
OTHER INFORMATION: unsure at all n locations
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SEQ ID NO 74236
LENGTH: 2085
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Best Local Similarity
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APPLICANT: Kovalic, David H
APPLICANT: Liu, Jingdong
APPLICANT: McInich, James
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50.5%;
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Pred. No. 3.
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PRIOR APPLICATION NUMBER: US 09/702,134
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
SEQ ID NO 86646
LENGTH: 3554
TYPE: DNA
ORGANISM: Oryza sativa
US-09-815-264-86646
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US-09-702-134-9663
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SEQ ID NO 9663
LENGTH: 3554
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Query Match 4.0%; Score 40.4; EBest Local Similarity 50.5%; Pred. No. 5.1; Matches 98; Conservative 0; Mismatches
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APPLICANT:
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APPLICANT: Wu, Wei
TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
FILE REFERENCE: 38-21(51237)G
CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
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CURRENT FILING DATE: 2000-10-31
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Wu, Wei
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McIninch, James
Wu, Wei
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Dotson, Stan
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Kovalic, David K.
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                 945 ggaagaacgaacgc 958
                                                                           885 agogtogcotocacogtocgtogotgccacototgctgtgcgcgcgcgcacgaaggga 944
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Search completed: September 12, 2002, 10:08:12 Job time: 9440 sec

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1: /cgn2_6/ptcdata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptcdata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptcdata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptcdata/2/pna/US08_NEW_COMB.seq:*

4: /cgn2_6/ptcdata/2/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptcdata/2/pna/US10_NEW_COMB.seq:*

6: /cgn2_6/ptcdata/2/pna/US10_NEW_COMB.seq:*

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8: /cgn2_6/ptcdata/2/pna/US10_NEW_COMB.seq:*
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7 US-10-155-881-23995
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7 US-10-179-131-253
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Sequence 1, Appli
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Sequence 10980, A
Sequence 25269, A
Sequence 213914,
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Sequence 13552, A
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Sequence 12490, Appli
Sequence 600, Appli
Sequence 482, Appli
Sequence 275, Appli
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Sequence 11, Appli
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Sequence 20130, A
Sequence 493, Appli
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RESULT 2
US-10-140-924-1
Sequence 1, Application US/10140924
Sequence 1, Application US/10140924
GENERAL INFORMATION:
APPLICANT: Gretarsdottir, Solveig
APPLICANT: Nonsdottir, Sif
APPLICANT: Reynisdottir, Sigridur Th.
TITLE OF INVENTION: HUMAN STROKE GENE
FILE REFERENCE: 2345.2010-000
CURRENT APPLICATION NUMBER: US/10/140,924
CURRENT FILING DATE: 2002-05-07
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; ORGANISM: Human
US-10-067-514-1
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                                                                                                         PCT-US02-25766-10980/c
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                                                    Sequence 10980, Application PC/TUS0225766 GENERAL INFORMATION:
APPLICANT: GENE LOGIC, INC.
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APPLICANT: Gretarsdottir,
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: US 09/811/352
PRIOR FILING DATE: 2001-03-19
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APPLICANT: Reynisdottir, Sigridur Th.
TITLE OF INVENTION: HUMAN STROKE GENE
FILE REFERENCE: 2345.2010-003
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Pred. No. 63;
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Pred. No. 71;
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; TYPE: DNA
; ORGANISM: Oryza
US-10-155-881-25269
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; NAME/KEY: misc_feature
; LOCATION: (1)..(6493)
; OTHER INFORMATION: n = a
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CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 37595
SEQ ID NO 25269
LENGTH: 691
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LENGTH: 6493
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APPLICANT: Lutflyya, Linda L.
APPLICANT: MCINICH, James
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
ETLE REFERENCE: 38-21 (15300)J
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PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 13946
SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5068-WO
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3393 TTGTTTTGAGACAGTCACATTCTATTTCTCAGGCTGGAGTGCAGGCATGATGATGGCTCG 3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3333 CTGAGGCCTCAACTTCCTGGGCTCAAGTAATCCT 3300
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                                                                 658 ttttttttacacgaaaatgccatagctggcccgcatgcgtgcagatcggatgatcggtcg 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      598 catgtacaaatacataatgtaccctacaatttgttttttggagcagagtgggtgtgggtctt 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    718 gagacgacggacaatcagacactcaccaactgct 751
                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81;
                                                                                                                71;
                                                                                                                                                                                                                                                                                                                                                                                                                         Novalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WAGA, Iwao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SASAI, Hitoshi
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                                                                                                                Conservative
                                                                                                                                                                                                            sativa
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                                                                                                                               3.6%;
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                                                                                                             Score 35.6; D
Pred. No. 11;
0; Mismatches
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                                                                                                                                              DB 7;
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US-10-027-632-213914
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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                                                                                                                                                                                                 Sequence 12, Application US/10201386
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                 CURRENT APPLICATION NUMBER: US/10/201,386 CURRENT FILING DATE: 2002-07-23 PRIOR APPLICATION NUMBER: US/09/534,376 PRIOR FILING DATE: 2000-03-24 PRIOR APPLICATION NUMBER: 09/355,700 PRIOR FILING DATE: 1999-11-05
                                                                                                                                            APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR C
TITLE OF INVENTION: AND GENE, MUTANTS THEREOF, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: PCT/US98/01973
                                                                                                                                          FILE REFERENCE: 28967/34140A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    948
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Local Similarity 49.4%;
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                                                                                                                                                                                                                                                                                                                                                                 ccaggaggattgcttgaacccgagattctgaggctgcaatgagctatgatcacactgctg 470
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Pred. No. 14;
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CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13552
LENGTH: 2407
TYPE: DNA
; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: 2407
; OTHER INFORMATION: n = A,T,C
US-10-198-846-13552
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; LCCATION: (453)..(1706)
; OTHER INFORMATION: Quail VEGF-C CDNA
US-10-201-386-12
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Best Local S
Matches 68
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APPLICANT: Lillie, James
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                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
FILE REFERENCE: MRI-049
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PRIOR FILING DATE: 1996-02-14
PRIOR APPLICATION NUMBER: 08/585,895
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PRIOR APPLICATION NUMBER: 08/510,133
PRIOR FILING DATE: 1995-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1996-08-01
PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1996-06-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/FI96/00427
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ORGANISM: Quail
                                                                                                    ORGANISM: Homo sapiens
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55.7%;
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RESULT 10
US-10-155-881-12490/c
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; ORGANISM: Oryza sativa
US-10-155-881-23995
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APPLICANT: Dotson, Stanton B.

APPLICANT: Kovalic, David K.

APPLICANT: Liu, Jingdong

APPLICANT: Lutfiyya, Linda L.

APPLICANT: McIninch, James
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; Sequence 23995, Application US/10155881
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Best Local s
Matches 99
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Lutflyya, Linda L.
APPLICANT: McIninch, James
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
FILE REFERENCE: 38-21(15300)J
CURRENT APPLICATION NUMBER: US/10/155,881
CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 37595
SEQ ID NO 12490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 37595
SEQ ID NO 23995
LENGTH: 774
                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                       Sequence 12490, Application US/10155881
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                                                                                                                                                                                            APPLICANT: Dotson, Stanton B. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2376 cagcgagacgcaaccgatcagcatg
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                                                                                                                                                                                                                                                                                                                                                   667 TTTTTTACAAAATTGGCAGATTAGACCCTGCTTTCC 632
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Local Similarity 60.4%;
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McIninch, James
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Pred. No. 21;
0; Mismatches 106;
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Pred. No. 15;
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APPLICANT: GREENE, JONATHAN R.
TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC AC
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 2976-4031
CURRENT APPLICATION NUMBER: US/10/179,131
CURRENT FILLING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 10194
SEQ ID NO 253
LENGTH: 2991
TYPE: DNA
US-09-053-375B-600/c

US-09-053-375B-600/c

; Sequence 600, Application US/09053375B

; GENERAL INFORMATION:

; APPLICANT: Chenchik, Alex
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US-10-155-881-12490
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Best Local Similarity 48.7
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APPLICANT:
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Best Local S
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                                                                                                      981 TAATAATTTGTCTCT
                                                                                                                                  621 ctacaatttgttttt 635
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NOLLING, JORK
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CURRENT APPLICATION NUMBER: US/09/053,375B CURRENT FILING DATE: 1998-08-31

APPLICANT: Bibilashvilli, Robert TITLE OF INVENTION: Nucleic Acid Arrays

FILE REFERENCE: CLON-006

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PCT-US02-09370-1049
; Sequence 1049, Application PC/TUS0209370
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
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Best Local Similarity
Matches 71; Conserva
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 600
LENGTH: 10495
TYPE: DNA
ORGANISM: Mus musculus
US-09-053-375B-600
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                                                                     RESULT 14
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Best Local Similarity 57.4%;
Matches 62; Conservative
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LENGTH: 15932
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NUMBER OF SEQ ID NOS: 779
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                                                                                                                                    606 aatacataatgtaccctacaatttgtttttttggagcagagtggtgtgg 653
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Pred. No. 71;
0; Mismatches
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Pred. No. 84;
0; Mismatches
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Search completed: September 12, Job time: 11174 sec

2002, 09:12:57

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Sequence 6415, Application US/10105299
GENERAL INFORMATION:
APPLICANT: Rosen, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS950
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                                                                                                                                                                                                                                                                                      Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 6415
LENGTH: 15932
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Best Local Similarity
Matches 62; Conserv
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SEQ ID NO 1049
LENGTH: 15932
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Best Local Similarity
                                                                                                                                              Matches
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CURRENT FILING DATE: 2002-03-26
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PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 09/950,083
PRIOR FILING DATE: 2001-09-12
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3960 cacacataaaggagactgtaaagaactttgggaggccgaggcaggtgg
                                                                        3900 gtgtaaaaaaacaaagacaatgtatatgtgaaatatgattccaattttatacatataca 3959
                                                                                          606 aatacataatgtaccctacaatttgttttttggagcagagtggtgtgg 653
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Pred. No. 84;
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Pred. No. 84;
                                                                                                                                                Mismatches
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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378 378 378 384 384 388	2017 3017 3017 724 7246 2446 2559 3039 21414 21414 21414	11463 104364 104364 416 102897 2853 2853 2368 2368 2368 2368 2368 2368 2368 236	Length
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sequence 1243, Ap Sequence 1240, Ap Sequence 424409, Sequence 454409, Sequence 454409,	385160 385160 385160 54797, 98960, 9, App 1, App 1, App 13950, 28820, 77542,	10, App 337, App 3, App	Description

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APPLICANT: MORELL, MATTHEW
APPLICANT: MORELL, MATTHEW
APPLICANT: MORELL, MATTHEW
APPLICANT: RAHMAN, SADEQUR
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS
FILE REFERENCE: 054270/0126
CURRENT APPLICATION NUMBER: US/09/508,377
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: AU PP 2509
PRIOR APPLICATION NUMBER: NO PP 2509
PRIOR APPLICATION NUMBER: NOT/AU98/00743
PRIOR APPLICATION NUMBER: AU PP 9108
PRIOR APPLICATION NUMBER: AU PP 9108
PRIOR APPLICATION NUMBER: OT/AU98/00743
PRIOR APPLICATION NUMBER: AU PP 9108
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: AU PP 9108
PRIOR FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PATENTIN Ver. 2.1
SOFTWARE: PATENTIN Ver. 2.1
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Matches 1001; Conserv
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US-60-207-458-97660
US-09-091-052-9
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US-09-931-052-1
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US-09-625-406-14
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Pred. No. 7.8e-231;
Mismatches 0;
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Conservative

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Indels

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LENGTH: 104364
TYPE: DNA
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       Query Match
Best Local Similarity
Matches 270; Conserv
                                                                                                                                                                                                                                                                         APPLICANT: Last, Robert L. APPLICANT: Levin, Irena M. APPLICANT: Norris, Susan F
                                                                                                                                                                      TITLE OF INVENTION: PLANT POLYMORPHIC FILE REFERENCE: 38-10(15493)B CURRENT PPLICATION NUMBER: US/09/534,859 CURRENT FILING DATE: 2000-03-29
                                                                                                                                                                                                                            APPLICANT: Parnell, Laurence D. APPLICANT: Rounsley, Steven D. APPLICANT: Wiegand, Roger C.
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                      14.18;
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         Score 141.2; I
Pred. No. 9.3e
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                      No. 9.3e-
DB 2(
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US-09-803-736-337; Sequence 337, Applic; GENERAL INFORMATION:
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/803,736
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 09/534,859
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: identified by A-
PRIOR FILING DATE: 2000-10-20
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APPLICANT: Wiegand, Roger C.
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EQ ID NO 337
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Norris, Susan R.
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APPLICANT:
APPLICANT:
Nucleic Acid M
TITLE OF INVENTION:
Nucleic Acid M
TITLE OF INVENTION:
Plants
FILE REFERENCE:
38-21(15877)B
CURRENT APPLICATION NUMBER: US/09/606,97
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS:
82359
SEQ ID NO 62778
LENGTH: 416
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Best Local Similarity
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; SEQ ID NO 1401
; LENGTH: 102897
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-1401
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                                                                             Sequence 3, Application 05,000.....
GENERAL INFORMATION:
GENERAL INFORMATION:
WILLMITZER, Lothar
APPLICANT: WICKGER, Christoph
THOMPTOKE, Stephan:
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Best Local Similarity 59.7
Matches 270; Conservative
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APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Plant Polymorphic Markers
FILE REFERENCE: 38-10(15493)D
CURRENT APPLICATION NUMBER: US/09/803,736
CURRENT FILING DATE: 2001-03-12
CURRENT FILING DATE: 2001-03-12
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APPLICANT: Levin, Irena
APPLICANT: Norris, Susar
APPLICANT: Rounsley, Ste
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: identified by Attorney Docket number 04983.0206CPUS01 38-10
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1582
APPLICANT: LUTTICKE, Ste
APPLICANT: LORZ, Horst
TITLE OF INVENTION: NUCL
TITLE OF INVENTION: THAN
TITLE OF INVENTION: IN F
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Norris, Susan R.
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                                                                         LUTTICKE, Stephanie
                                                                                                                WILLMITZER, Lothar
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59.78;
NUCLEOTIDE SEQUENCES ENCODING ENZYMES
THAT ALTER THE CARBOHYDRATE CONCENTRATION AND COMPOSITION
IN PLANTS
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Pred. No. 1.9e-
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APPLICATION NUMBER: DE P
FILING DATE: 13-FEB-1991
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 382-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 13-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward
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 1117
                                                           1057
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ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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LENGTH: 2853 base pairs
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                             433
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP PO
FILING DATE: 11-FEB-1992
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                                                                                                                                                                                                                                                                           LOCATION:
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                                                          AGGCTTGGATACAATGCAGTGCAGATAATGGCAATCCAGGAGCATTCATACTATGCAAGC
                                                                        aggcttggatacaatgcagtgcagataatggcaatccaggagcattcatactatgcaagc 432
                          tttgggtattcacacaatccattttttc
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SYSTEM: PC-DOS/MS-DOS
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91.3%;
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; Sequence 3, Application US/09609040 ; GENERAL INFORMATION:

US-09-609-040-3

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; LOCATION: (313)..(2499)
; OTHER INFORMATION: BRANCHING ENZYME
US-09-609-040-3
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Best Local S
Matches 159
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Best Local Similarity
Matches 136; Conserv
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APPLICANT:
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TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATE
TITLE OF INVENTION: CONCENTRATION AND COMPOSITION IN PLANTS
EILE REFERENCE: 514413-5515.1

CURRENT APPLICATION NUMBER: US/09/609,040

CURRENT FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: PCT/EP92/00302

PRIOR APPLICATION NUMBER: PCT/EP92/00302

PRIOR FILING DATE: 1992-02-11

NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liu, Jingdong
APPLICANT: McIninch, James
TITLE OF INVENTION: P
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TYPE: DNA
ORGANISM: Triticum aestivum
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                                                                                                                                                                               Local Similarity 75.4
mes 159; Conservative
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               aatccttgatcgatagagcacatgagcttggtttgcttgttcttatggatattgttcata
                                                          GGTATCATGTTACTAACTTCTTTGCGCCAAGTAGCCGTTTCGGAACCCCAGAAGACTTGA
                                                                           ggtaccatgttactaatttttttgcaccaagtagccgttttggaactccagaggacttaa
                                                                                                                    ATAGTGCAACTATTCTTTCTGTTTCTGACCTGGTTTGATCTTTGTTATATTCTTTTTACA 2256
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AATCTCTGATTGATAAAGCTCACGAGCTTGGTTTGCTTGTACTTATGGATATTGTTCACA
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                                                                                                                                                                                           12.8%;
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91.3%;
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Pred. No. 4.5e-20;
0; Mismatches 52;
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Pred. No. 3.8e-20;
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 TYPE: DNA
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CURRENT APPLICATION NUMBER: US/09/702,134

CURRENT FILING DATE: 2000-10-31

NUMBER OF SEQ ID NOS: 52202

SEQ ID NO 20657

LENGTH: 2368

TYPE: DNA

OGRANIZSM: OTYZA SATIVA
US-09-702-134-20657
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 91233, Application US/09815264 GENERAL INFORMATION:
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SEQ ID NO 91233
LENGTH: 2368
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Best Local Similarity
                                                                                                                                APPLICANT: Wu, Wei
TITLE OF INVENTION: Genomic Plant Sequences
FILE REFERENCE: 38-21(51237)G
CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
CURRENT FILING DATE: 10 00.6707 392
                                  PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/702,134
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Boukharov, Andrey A. APPLICANT: Cao, Yongwei APPLICANT: Dotson, Stanton B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2315 ATAGTGCAACTATTCTTTCTGTTTCTGACCTGGTTTGATCTTTTGTTATATTCTTTTTACA 2256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aatccttgatcgatagagcacatgagcttggtttgcttgttcttatggatattgttcata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTATCATGTTACTAACTTCTTTGCGCCCAAGTAGCCGTTTCGGAACCCCCAGAAGACTTGA 2196
                                                                                                                                                                                                                                                                                       Dotson, Stanton B
Koshi, Jeffrey M.
Kovalic, David K.
                                                                                                                                                                                                                                               McIninch, James
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                                                                                                                                                                                                                                                                     Liu, Jingdong
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Pred. No. 4.5e-20;
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; ORGANISM: Oryza sativa
US-09-572-409-26244
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US-09-815-264-91233
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PRIOR FILING DATE:
NUMBER OF SEQ ID NOS:
SEQ ID NO 26644
LENGTH: 400
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Best Local Similarity
Matches 200; Conserv
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Best Local Similarity
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TITLE OF INVENTION: Plants
38-21(15860)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/572,409
CURRENT FILING DATE: 2000-05-16
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 304
                            756 ttt 758
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tct
                                                                        tggtttgcttgttcttatggatattgttcataggtaattagtccaaatttaattttagctg
                                                                                                                aagtagccgttttggaactccagaggacttaaaatccttgatcgatagagcacatgagct 695
                                                                                                                                                                                       aaagatcattttattgttggttggcttgttccaggtaccatgttactaatttttttgcacc 635
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                                                      tggtttgcttgtacttatggatattgatcacaggtaattagcgaaatggtgatttgttcg
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306
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79201
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                                                                                                                                                                                                                                                                                                                                              Score 126.6; DB 22;
Pred. No. 4.8e-20;
Pred. No. 4.8e-20;
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Pred. No. 4.5e-20;
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; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3399-050-P1-K1-H8
US-60-189-657-14485
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-60-189-657-14485; Sequence 14485, Appl; GENERAL INFORMATION:
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US-09-804-730-16419
                                                                                                                                                                                           TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: PLANT'S FILE REFERENCE: 38-21(51838)A CUBRENT APPLICATION NUMBER: US/60/189,657 CURRENT FILING DATE: 2000-03-15 NUMBER OF SEQ ID NOS: 22822 SEQ ID NO 14485 LENGTH: 345
Query Match
Best Local Similarity
Matches 132; Conserv
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Best Local Similarity
Matches 132; Conserv
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LENGTH: 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/189,657
PRIOR FILING DATE: 2000-03-15
NUMBER OF SEQ ID NOS: 22828
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TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5,1838)B
CURRENT APPLICATION NUMBER: US/09/804,730
CURRENT FILING DATE: 2001-03-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     436 gggtattcacacaatccatttttttc 461
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    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/60189657
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                    12.3%;
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Score 123.6; DB 57
Pred. No. 2.4e-19;
0; Mismatches 14;
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Pred. No. 2.4e-19;
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                                       DB 57;
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                                       Length 345;
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APPLICANT: Kim, Kyung-Nam
TITLE OF INVENTION: Expression Control Elements from Genes
TITLE OF INVENTION: Expression Control Elements from Genes
TITLE OF INVENTION: Encoding Starch Branching Enzymes
FILE REFERENCE: Encoding Starch Branching Enzymes
FILE REFERENCE: Encoding Starch Branching Enzymes
FURRENT FILING DATE: 1990-06-11
PRIOR APPLICATION NUMBER: US 60/089,049
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: US 60/089,050
PRIOR FILING DATE: 1998-06-12
PRIOR TILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                US-09-887-272A-4612; Sequence 4612, Application US/09887272A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFIWALL
SEQ ID NO 2
- THOTH: 23449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gequence 2. Application US/09330889A
GENERAL INFORMATION:
APPLICANT: Guiltinan, Mark A.
APPLICANT: Kim, Kyung-Nam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                             APPLICANT: APPLICANT:
                                          APPLICANT:
                                                                                                                                                                                                                                                           APPLICANT: Hou, Yu-Ming
                                                                                                                                                                                                                                                                                                                                                                                             7705 aagctttgggtaatttcaggatccagttttgtttgtct 7742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7585 tgattaggaaccgaagataaacacatatgtaaactttagggatgaagtcctcccaagaat 7644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7645 aaaaaaacttggatacaatgcagtgcaaataatggcaatccaagagcactcatattatgg 7704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369 taaaaggcttggatacaatgcagtgcagataatggcaatccaggagcattcatactatgc 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309
                                                                                                                                                                                                                                                                                                                                                                                                                    429 aagctttgggtattcacacaatccatttttttctgtat 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gggtaccatgttactaatttttttgc 190
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TOOPER, Bret INVOLVED IN DEFENSE AGAINST
                                                                                             Goff, Steve
Glazebrook, Jane
Chen, Wenquiong
Katagiri, Fumiaki
                                                                                                                                                                           Quan, Sheng
Chang, Hur-Song
Zhu, Tong
Whitham, Steve
                                        Zou,
                                                             Tao,
                                                                             Xie,
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                                      Guangzhou
                                                                             Zhiyi
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81.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 23449;
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                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 124; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 6813
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4612
LENGTH: 2655
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PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/273,879
PRIOR FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 09/887,271
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/214,926
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/261,320
PRIOR FILING DATE: 2001-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/887,272A
CURRENT FILING DATE: 2001-06-23
PRIOR APPLICATION NUMBER: 60/213,634
PRIOR FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: FILE REFERENCE: 1360
                                                                                                                                                                                     1093 ccggaaccgaagataaacacatatgctaattttagggatgaggtgctaccaagaattaaa 1152
                                                                                            1153 aagettgggtacaatgetgtacagataatggeaateeaggageaetettattaegeaage 1212
                       433 tttgggtattcacacaatccatttttttc 461
                                                                                                                    373 aggcttggatacaatgcagtgcagataatggcaatccaggagcattcatactatgcaagc 432
                                                                                                                                                                                                          313 caggaaccgaagataaattcatatgctaattttagggatgaggtgttgccaagaattaaa 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE: 1360.003US2
tttgggtatcatgttactaacttctttgc 1241
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                             10.9%; Score 109; DB 33; 83.2%; Pred. No. 1.6e-15; ative 0; Mismatches 25;
                                                                                                                                                                                                                                                                                                                        Length 2655;
                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                             Gaps
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Search completed: September 12, 2002, 10:11:16 Job time: 9624 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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IDENTITY_NUC Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pending_Patents_NA_Main: *
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Copyright (c) 1993 - 2000 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score

Match Length DB

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Description

Query

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117.8 117.8 117.8 117.8	120.4 120.4 120.4 120.4 118.8	120.4 120.4 120.4 120.4 120.4	122 122 122 122 122 122	187.2 136.4 134.8 134.8 128.8	1001 223.2 187.2 187.2
11.8 11.8 11.8		12.0 12.0 12.0 12.0	12.22	18.7 13.6 13.5 13.5	100.0 22.3 18.7 18.7
3017 413 413 567	441 441 441 527 3017	2446 399 399 399 441	420 420 421 421 531 531	21414 1119 2853 2853 2655	11463 23449 21414 21414
17 22 32	17 22 36 17 25	27 27 27 27 27 27 27 27 27 27 27 27 27 2	17 17 17 17 17 17 32	31 71 11 23 33	19 17 24 28
US-09-884-016-385160 US-09-394-745-48567 US-09-565-306-69979 US-09-849-526A-2386	563953 573859	US-09-637-086A-1807 US-09-637-086D-1807 US-09-634-617-204100 US-09-654-617-204100 US-09-304-517A-93092	US-09-304-517A-91564 US-09-985-678-91564 US-09-394-745-21714 US-09-565-306-42955 US-09-371-146A-91564 US-09-849-526A-2236 US-60-202-214-2236	99-09	US-09-508-377-10 US-09-330-889A-2 US-09-620-392-13950 US-09-702-134-28820
Sequence 385160, Sequence 48567, A Sequence 69979, A Sequence 2386, Ap		9, APP1 1807, A 1807, A 204100, 204100, 93092,	Sequence 91564, A Sequence 91564, A Sequence 21714, A Sequence 42955, A Sequence 91564, A Sequence 2336, Ap Sequence 2336, Ap	Sequence 77542, A Sequence 3410, Ap Sequence 3, Apppli Sequence 3, Appli Sequence 4612, Ap	Sequence 10, Appl Sequence 2, Appli Sequence 13950, A Sequence 28820, A

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; SEQ ID NO 10
; LENGTH: 11463
; TYPE: DNA
; ORGANISM: Triticum t
US-09-508-377-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KALEEN, ZHONGYILI
APPLICANT: MORELL, MATTHEW
APPLICANT: MARTHEW
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN
FILE REFERENCE: 054.270/0126
CURRENT APPLICATION NUMBER: US/09/508,377
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: AU PP 2509
PRIOR APPLICATION NUMBER: BUP 2509
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PT/AU98/00743
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: AU PP 9108
PRIOR FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 71
SECO ID NOS: 71
SECO ID NOS: PATENTIN PET. 2.1
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US-09-508-377-10
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Best Local Similarity
Matches 1001; Conserv
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US-09-850-147-7191
US-60-202-213-7178
US-09-850-147-4345
US-09-850-147-4345
US-09-684-617-452844
US-09-684-016-452844
US-09-667-188A-2250
US-60-155-006-3134
US-09-667-188A-1619
US-09-667-188A-1619
US-09-667-188A-1649
US-09-667-188A-1639
US-60-155-006-2503
US-09-350-147-6476
US-60-202-213-6463
US-09-304-517A-49291
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Pred. No. 3.2e-231;
Mismatches 0;
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                                        NUMBER: FASTSE
SOFTWARE: FASTSE
; SEQ ID NO 2
FENGTH: 23449
                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09330889A GENERAL INFORMATION:
                                                                                                                                                                                  APPLICANT: Guiltinan, Mark A.

APPLICANT: Kim, Kyung-Nam
TITLE OF INVENTION: Expression Control Elements from Genes
TITLE OF INVENTION: Encoding Starch Branching Enzymes
FILE REFERENCE: Penn State 1465
CURRENT APPLICATION NUMBER: US/09/330,889A
CURRENT FILING DATE: 1999-06-11.
                                                                               PRIOR APPLICATION NUMBER: US 60/089,049
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: US 60/089,050
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4
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Query Match
Best Local Similarity
Matches 649; Conserv

Conservative

22.3%;

Score 223.2; DB 1 Pred. No. 6.3e-43; 0; Mismatches 333

DB 17;

Length 23449;

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                                         cggaaacatgaggaagataaggtgatcatcctcaaaagaggagatttggtatttgtttc
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                                                                                             catataccagcactgacaatgtaactgcagtttatgacatctgagcaccagtatgtttca
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FILE REFERENCE:

Plant Genome Sequence And FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/620,392

CURRENT FILING DATE: 2000-07-19

NUMBER OF SEQ ID NOS:

SEQ ID NO 13950

LENGTH: 21414

TYPE: DNA

ORGANIEM: OTYZEA SATÍVA

US-09-620-392-13950
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                                                                                                                                                                       US-09-702-134-28820/c
                                                                                                                                   Sequence 28820, Application US/09702134 GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
APPLICANT:
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Best Local Similarity
Matches 306; Conserv
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APPLICANT: McIninch, James
TITLE OF INVENTION: P
              APPLICANT: Wu, Wei
TITLE OF INVENTION:
                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                           GTANA-TTCATCCCAGGGAATAACAACAGTTATGATAAATGCCGTCGAAGATTTGACCTG 10363
                                                                                                                                                                                                                                                                                                                           gcaaagttctcccctggaaataacaatagttatgataaatgccgccgtagatttgatctt
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                                                                                                   Cao,
                                              McIninch, James
                                                                Liu, Jingdong
                                                                                Kovalic, David K
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nilarity 71.5%;
Conservative
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                                                                                                Yongwei
                                                                                                                   Boukharov, Andrey
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Plant Genome
38-21(51237)F
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                Sequence
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TITLE OF INVENTION: Genomic Plant Sequences And Use FILE REFERENCE: 38-21(51237)G
CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
SEQ ID NO 77542
LENGTH: 21414
TYPE: DNA
; ORGANISM: Oryza sativa 
US-09-815-264-77542
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; ORGANISM: Oryza sativa
US-09-702-134-28820
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GENERAL INFORMATION:
APPLICANT: Boukharov, Andrey A.
APPLICANT: Cao, Yongwei
APPLICANT: Dotson, Stanton B.
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Best Local Similarity
Matches 306; Conserv
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CURRENT FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 52202
SEQ ID NO 28820
LENGTH: 21414
                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
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Koshi, Jeffrey M.
Kovalic, David K.
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McIninch, James
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71.5%;
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; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Triticum a
                                                                                                                                                                             Query Match
Best Local Similarity
Matches 148; Conserv
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Best Local Similarity 71.5%;
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/60/325,448
CURRENT FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 4708
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Budworth, P.R. APPLICANT: Moughamer, T.
                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 1360.026PRV
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Moughamer, T.G.
TITLE OF INVENTION: Constitutive rice
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                                                                                                                                43 aggatatgtatgatttcatggctctggatagg-cttcaactcttcgccattgatcgtggca 101
              acttcatgggaaatgagtttgggcatcctg
                                                                      tagcattacataaaatgatcaggcttgtcaccatgggtttaggtggtggaggctatctta 161
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Pred. No. 2.5e-22;
0; Mismatches 1;
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; LOCATION:
US-08-726-705-3
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,705
FILING DATE: 07-OCT-1996
CLASSIFICATION B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,158
FILING DATE: 13-AUG-1993
                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 236925 ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP PCT/EP92/0030
FILING DATE: 11-FEB-1992
PRIOR APPLICATION UMBER: DE P 41 04 782.6
FILING DATE: 13-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUCLECTIDE SEQUENCES ENCODING ENZYMES
TITLE OF INVENTION: THAT ALTER THE CARBOHYDRATE CONCENTRATION AND COMPOSITION
TITLE OF INVENTION: IN PLANTS
                                   1859 AGGATATGTATGATTTCATGGCTCTGGATAGGCCTTCAACTCCTCGCATTGATCGTGGCA 1918
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 382-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
102 tagcattacataaaatgatcaggcttgtcaccatgggtttaggtggtgaaggctatctta 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1180 A:
CITY: New York
                                                    43 aggatatgtatgatttcatggctctggatagg-cttcaactcttcgcattgatcgtggca 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                           ORGANISM:
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                                                                                                       147;
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1180 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                             2853 base pairs
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                                                                                                  Score 134.8; DB 11;
Pred. No. 8.1e-22;
0; Mismatches 2;
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; NAME/KEY: CDS
; LOCATION: (313)..(2499)
; OTHER INFORMATION: BRANCHING ENZYME
US-09-609-040-3
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Best Local Similarity
Matches 147; Conserv
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                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                               APPLICANT: ZOU, Guangzhou
APPLICANT: COOper, Bret
TITLE OF INVENTION: PLANT GENES INVOLVED IN DEFENSE AGAINST
TITLE OF INVENTION: PATHOGENS
FILE REFERENCE: 1360.003US2
                                                                                                                                                       APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/887,272A CURRENT FILING DATE: 2001-06-23
                                                                                                                        APPLICANT:
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                                                                                                  Tao, Yi
Zou, Guangzhou
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Katagiri, Fumiaki
                                                                                                                                                                                           Glazebrook, Jane
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m, Steve
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Pred. No. 8.1
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CURRENT APPLICATION NUMBER: US/09/304,517A
CURRENT FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 295529
SEQ ID NO 91564
LENGTH: 420
TYPE: DNA
OCANISM: Zea mays
US-09-304-517A-91564
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Best Local Similarity 84.8
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SEQ ID NO 4612
LENGTH: 2655
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Best Local
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APPLICANT: Liu, Jingdong
TITLE OF INVENTION:
FILE REFERENCE: 38-2
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PRIOR FILING DATE: 2001-03-07
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les 139; Conserv
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acttcatgggaaatgagtttgggcatcctg 191
                                             tagcattacataaaatgatcaggcttgtcaccatgggtttaggtggtgaaggctatctta 161
                                                                             tagcattacataaaatgattaggcttgtcacaatgggtttaggaggtgaaggctatctaa
                                                                                                                           Conservative
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                                                                                                                          Score 122; DB 17;
Pred. No. 5.7e-19;
0; Mismatches 10;
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Pred. No. 2.2e-20;
Pred. No. 2.7e-20;
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                                                                                                                                                Length 420;
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APPLICANT: Cheikh, Nordine
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 16517.255/38-21(15097)F
CURRENT APPLICATION NUMBER: US/09/985,678
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: US 09/304,517
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 295529
SEQ ID NO 91564
LENGTH: 420
                                                                                                                                                                                                                                  ; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3062-002-Q1-K2-E10
US-09-394-745-21714
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US-09-985-678-91564
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LENGTH: 421
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Best Local Similarity
                                                                                                                                                           Matches 139; Conservative
                                                                                                                                                                        Query Match
Best Local Similarity
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CURRENT FILING DATE: 1999-09-15
NUMBER OF SEQ ID NOS: 57264
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fisher, Dane K. APPLICANT: Lalgudi, Raghunath V. TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                    TYPE: DNA
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pred. No. 5.7e-19;
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Pred. No. 5.7e-19;
0; Mismatches 10;
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APPLICANT: Conner, Timothy W.

APPLICANT: Lalgudi, Raghunath V.

TITLE OF INVENTION: Nucleic Acid Molec

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15459)C

CURRENT APPLICATION NUMBER: US/09/565,306

CURRENT FILING DATE: 2000-05-04

NUMBER OF SEQ ID NOS: 83523

SEQ ID NO 42955

LENGTH: 421
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; LCATION: (1)..(499)
; OTHER INFORMATION: unsure at all n locations
US-09-371-146A-91564
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Best Local Sin
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Matches 139
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LENGTH: 499
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APPLICANT: Liu, Jingdong
TITLE OF INVENTION: ANNOTATED PLANT GENES
FILE REFERENCE: 38-21(15097)C
CURRENT APPLICATION NUMBER: US/09/371,146A
CURRENT FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/304,517
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 294310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                         TYPE: DNA
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acttcatgggaaatgagtttgggcatcctg 191
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92.7%;
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Pred. No. 5.7e-19;
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Pred. No. 6e-19;
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                                                                                           DB 17; Length 499;
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Search completed: September 12, Job time: 9689 sec

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SEQ ID NO 2236
LENGTH: 531
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 16517.250[38-21(51930)B] CURRENT APPLICATION NUMBER: US/09/849,526A CURRENT FILING DATE: 2001-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/202,214
PRIOR FILING DATE: 2000-05-08
PRIOR PPLICATION NUMBER: US 09/654,617
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 09/684,016
PRIOR FILING DATE: 2000-10-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/816,660 PRIOR FILING DATE: 2001-03-26
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                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays subsp. mexicana
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               acttcatgggaaatgagtttgggcatcctg 191
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                                                                                           tagcattacataaaatgatcaggcttgtcaccatgggtttaggtggtgaaggctatctta 161
                                                                                                                                                139;
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

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5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*

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US-10-056-454A-17
US-10-056-454A-14
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US-10-110-777-1
US-10-110-777-1
US-60-368-387-2
US-60-360-039-33970
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Sequence 1, Appli Sequence 1, Appli	Sequence 1616, Ap Sequence 1, Appl	Sequence 8524, A Sequence 152, Ap	Sequence 14448, A Sequence 2345, Ap	Sequence 601, App	Sequence 1, Appli	Sequence 76212,	Sequence 39, Appl	Sequence 28, Appl	Sequence 214, App	Sequence 1226, Ap	Sequence 375, App	Sequence 8, Appl.	Sequence 29078,	Sequence 16738,	Sequence 25407,

ALIGNMENTS

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Sequence 1. Application US/10162948

GENERAL IMPORMATION:
APPLICANT: Jane, Jay-lin
APPLICANT: Mou Beiquan
APPLICANT: Mou Beiquan
APPLICANT: Mou Beiquan
APPLICANT: Mou Beiquan
APPLICANT: Sun, Chuanxin
TITLE OF INVENTION: TRANSGENIC CORN PLANTS HAVING SEEDS WITH MODIFIED
TITLE OF INVENTION: TRANSGENIC CORN PLANTS
FILE REFERENCE: 48927, 90081
CURRENT APPLICATION NUMBER: US/10/162,948
CURRENT FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 00/295,649
PRIOR APPLICATION ONMOBER SO/295,649
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2554
TYPE: DNA
ORGANISM: Hordeum vulgare
FEATURE:
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US-10-162-948-1
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Best Local Similarity
Matches 144; Conserv
        1688
                                                                                                                                                             1568 aggatatgtatgatttcatggctctggatagaccttcaacccctcgcattgatcgtggca 1627
                                                                              1628 tagcattacataaaatgatcaggcttgtcaccatgggtttaggtggcgaaggctatctta
                        162 acttcatgggaaatgagtttgggcatcctg 191
                                                                                                       102 tagcattacataaaatgatcaggcttgtcaccatgggtttaggtggtgaaggctatctta 161
                                                                                                                                                                                43 aggatatgtatgatttcatggctctggatag-gcttcaactcttcgcattgatcgtggca 101
atttcatgggaaatgagtttgggcatcctg 1717
                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                          Score 130; DB Pred. No. 5.5e 0; Mismatches
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.5e-23;
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RESULT 2 US-60-391-781-685 ; Sequence 685, Application US/60391781

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                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; LOCATION: (1)..(2443)
; OTHER INFORMATION: SBEII modified region
US-60-368-387-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/60368387
GENERAL INFORMATION:
APPLICANT: Pearlstein, Richard W.
APPLICANT: Broglie, Karen E.
APPLICANT: Hines, Christopher F.
TITLE OF INVENTION: Maize Starch Containing Elevated Amounts of Actual Amylose
FILE REFERENCE: BB1510PRY
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APPLICANT: Laurie, Cathy C.

TITLE OF INVENTION: Nucleic Acid Molecules Associated With Oil
FILE REFERENCE: 38-77(52900)B

CURRENT APPLICATION NUMBER: US/60/391,781

CURRENT FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR APPLICATION NUMBER: 60/365,301

PRIOR FILING DATE: -2002-03-15

NUMBER OF SEQ ID NOS: 3034

SEQ ID NO 685

LENGTH: 3144
                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 132; Conserv
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SEQ ID NO 1
LENGTH: 2443
TYPE: DNA
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CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
     1531
                                                                                                                                          1411 aggatatgtatgatttcatggccctcgatagaccttcaactcctaccattgatcgtggga 1470
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88.0%;
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Pred. No. 4.1e-18;
0; Mismatches 17
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Pred. No. 6.3e-21;
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PRIOR APPLICATION NUMBER: 60/365,301
PRIOR FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 3034
SEQ ID NO 709
LENGTH: 2919
TYPE: DNA
ORGANISM: Zea mays
US-60-391-781-709
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; LOCATION: (1)..(2443)
; OTHER INFORMATION: SBEII modified region
US-60-381-534-1
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; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C.
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Oil in Plants
; FILE REFERENCE: 38-77(52900)B
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Best Local Similarity
Matches 132; Conserv
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Best Local Similarity 88.0%;
Matches 132; Conservative
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CURRENT FILING DATE: 2002-06-25
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APPLICANT: Hines, Christopher F.
TITLE OF INVENTION: Maize Starch Containing Elevated Amounts of Actual Amylose
FILE REFERENCE: BB1510PRV1
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
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CURRENT FILING DATE: 2002-05-16
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ORGANISM: Artificial Sequence
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102 tagcattacataaaatgatcaggcttgtcaccatgggtttaggtggtgaaggctatctta 161
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ilarity 88.0%;
Conservative
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Pred. No. 4.1e-18;
0; Mismatches 17;
                                                                                                                                                    Score 110.8; DB 8; Pred. No. 4.3e-18; 0; Mismatches 17;
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PRIOR APPLICATION NUMBER: 60/365,301
PRIOR FILING DATE: 2002-03-25
PRIOR FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 3034
SEQ ID NO 2614
LENGTH: 786
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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US-10-056-454A-12
; Sequence 12, Application US/10056454A
; GENERAL INFORMATION:
GENERAL INFORMATION:
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; LICATION: (1)..(786)
; OTHER INFORMATION: unsure at all n locations
US-60-391-781-2614
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Best Local (
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TITLE OF INVENTION: Nucleic Acid Molecules
FILE REFERENCE: 38-77(52900)B
CURRENT APPLICATION NUMBER: US/60/391,781
CURRENT FILING DATE: 2002-06-25
                                                                                        APPLICATION NUMBER: US/10/056,454A FILING DATE: 25-Jun-2002 INFORMATION FOR SEQ ID NO: 12:
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                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: National Starch and Chemical Investment Holding Corporation TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: National Starch
STREET: 1000 Uniqema Blvd.
              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                            STATE: Delaware
                                                                                                                                                                                                                                                                                                                            CITY: Newcastle
TOPOLOGY: linear
                                                    LENGTH: 3003 base pairs
                                                                                                                                                                                                                                                                                      COUNTRY: United States of America
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Pred. No. 3.6e-16;
0; Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                                            Chemical Investment Holding Corporation
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                                                                                                                                                                       Version #1
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RESULT 9
US-10-056-454A-14
; Sequence 14, Application US/10056454A
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US-10-056-454A-17
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/056,454A FILING DATE: 25-Jun-2002 INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2187
                                                                                                   1958
                                                                                                                                                                              1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2127 GATCGTGGGATAGCATTACACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAA 2186
                                                                                                                                                                                                                                                      1838 CTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGYCAACAYCATTAATA 1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2067 CTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATA 2126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 ggctatcttaacttcatgggaaatgagtttgggcatcctg 191
                                                                                                                                         152
                                                                                                                                                                                                92 gatcgtggcatagcattacataaaatgatcaggcttgtcaccatgggtttaggtggtgaa 151
                                                                                                                                                                                                                                                                          33 ctctttgtgcaggatatgtatgatttcatggctctggatag-gcttcaactcttcgcatt 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: National Starch and Chemical Investment Holding Corporation TITLE OF INVENTION: Improvements in or Relating to Plant Starch Compos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125;
                                                                                                                   ggctatcttaacttcatgggaaatgagtttgggcatcctg 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTG
                                                                                                                                                                              GATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAA 1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Delaware COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: National Starch
STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Newcastle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2529 base pairs
                                                                                                                                                                                                                                                                                                                                  Conservative
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78.18;
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                                                                                                                                                                                                                                                                                                                              Score 92.8; DB 7;
Pred. No. 1.6e-13;
2; Mismatches 34;
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Pred. No. 1e-13;
0; Mismatches 34; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version
                                                                                                     1997
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                                                                                                                                                                                                                                                                                                                                                                 Length 2529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
ETILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2188 GGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTG 2227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2128 GATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAA 2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2068 CTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGTCAACATCATTAATA 2127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 ggctatcttaacttcatgggaaatgagtttgggcatcctg 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 gatcgtggcatagcattacataaaatgatcaggcttgtcacccatgggtttaggtggtgaa 151
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Local Similarity 77.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 ctctttgtgcaggatatgtatgatttcatggctctggatag-gcttcaactcttcgcatt 91
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: National Starch and Chemical Investment Holding Corporation TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 145..2790
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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ADDRESSEE: National Starch and Chemical Investment Holding Corporation
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Improvements NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: National Starch and Chemical Investment Holding Corporation TITLE OF INVENTION: Improvements in or Relating to Plant Starch Compos
                                                                                                                                                                                                                                                                                                            ADDRESSEE: National Starch and Chemical Investment Holding Corporation STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                              COUNTRY: United States of America
                                                                                                                                                                                                                                                                        STATE: Delaware
                                                                                                                                                                                                                                                                                            CITY: Newcastle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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                                                                                                                                                                              MEDIUM TYPE: Floppy disk
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Pred. No. 2.6e-13;
Pred. No. 35;
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; Sequence 19, Application US/10056454A
; GENERAL INFORMATION:
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Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     1845 CTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGCCAACATCATTAATA 1904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1963 GGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1843 CTGATGGACAAGGATATGTATGATTTTATGGCTCTGGATAGACCGCCAACATCATTAATA 1902
                             1965 GGGTACCTAAATTTCATGGGAAATGAATTCGGCCACCCTG
                                                                                                                1905 GATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAA 1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1903 GATCGTGGGATAGCATTGCACAAGATGATTAGGCTTGTAACTATGGGATTAGGAGGAGAA 1962
                                                  152 ggctatcttaacttcatgggaaatgagtttgggcatcctg
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                                                                                                                                  92 gatcgtggcatagcattacataaaatgatcaggcttgtcaccatgggtttaggtggtgaa 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIAL #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19720
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: National Starch and Chemical Investment Holding Corporation
STREET: 1000 Uniqema Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Improvements in or Relating NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: National Starch and Chemical Investment
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2576 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Newcastle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2578 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 25-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America
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Pred. No. 6.3e-13;
0; Mismatches 36;
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Corporation

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RESULT 13
US-10-056-454A-18
US-10-056-454A-18
; Sequence 18, Application US/10056454A
; GENERAL INFORMATION:
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US-10-056-454A-13
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GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment Holding Corporation
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Compos
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Best Local S
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILING DATE: 25-Jun-2002
                                                                CURRENT
                                                                                                                                                                     ZIP: 19720
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: National Starch and Chemical Investment Holding Corporation TITLE OF INVENTION: Improvements in or Relating to Plant Starch Compos
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LENGTH: 2975 base pairs
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STATE: Delaware
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STREET: 1000 Uniqema Blvd.
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STRANDEDNESS: single
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INT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,454A
FILLNG DATE: 25-Jun-2002
IN FOR SEQ ID NO: 18:
                                                                               MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STATE: Delaware
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Pred. No. 6.6e-13;
0; Mismatches 36
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TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-15
PRIOR FILING DATE: 2001-09-15
PRIOR FILING DATE: 2001-08-15
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LENGTH: 1867
TYPE: DNA
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Best Local Similarity
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OTHER INFORMATION:
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LOCATION: (3)
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670 attttatggggaatgaatttggccatcctg
                                                                                        102 tagcattacataaaatgatcaggcttgtcaccatgggtttaggtggtgaaggctatctta 161
                                                                                                                                              550 aggatatgtatgacttcatggctttagacagaccatccacacctattatagatcgtggta 609
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LENGTH: 3231 base pairs
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                   tagcgttgcacaaaatgattaggcttattaccatgggtcttggtggtgaagggtatttaa 669
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Hinkle, Gregory J
Kovalic, David K.
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Pred. No. 6.8e-13;
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RESULT 15
US-10-213-073-149
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OR FILING DATE: 2001-01-16
OR APPLICATION NUMBER: 60/179,065
OR FILING DATE: 2000-01-31
OR APPLICATION NUMBER: 60/180,628
OR FILING DATE: 2000-02-04
OR APPLICATION NUMBER: 60/214,886
OR FILING DATE: 2000-06-28
OR APPLICATION NUMBER: 60/217,487
OR APPLICATION NUMBER: 60/217,487
OR APPLICATION NUMBER: 60/217,487
OR APPLICATION NUMBER: 60/225,758
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/220,963
OR FILING DATE: 2000-07-26
OR APPLICATION NUMBER: 60/217,496
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OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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APPLICATION N
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                                       NUMBER: 60/225,268: 2000-08-14
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NUMBER: 60/
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OR FILING DATE: 2000-10-02
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KEYWORDS
SOURCE
ORGANISM
Acgilops tauschii.
CORGANISM
Acgilops tauschii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Endryota; Pooldeae; Triticeae; Aegilops.

REFERENCE
AUTHORS
TITLE
JOURNAL
Regulation of gene expression in plants
Pooldman FIELDER LTD (AU); LT ZHONGYI (AU); MORELL MATTHEW (AU);
RAHMAN SADEQUR (AU); ONIV AUSTRALIAN (AU); COMMW SCIENT IND RESSOURCE
ORG (AU); GROUPE LIMAGRAIN PACIFIC PTY L (AU)

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Rahman,S., Regina,A., Li,Z., Mukai,Y., Yamamoto,M., Kosar-Hashemi,B., Abrahams,S. and Morell,M.K.
Comparison of Starch-Branching Enzyme Genes Reveals Relationships Among Isoforms. Characterization of a Starch-Branching Enzyme IIa from the Wheat D Genome
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Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Aegilops.
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HTG; HTGS_PHASE1; HTGS_I
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
1 (bases 1 to 225726)
Smith, D. R.
                                                                                                                    AC074328 225726 bp II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 210476)
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                                                     Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence Data
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                                                                 house mouse.
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                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP23-354D10"
/clone_lib="RPCI-23"
41038 c 40306 g 64759
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                                                                              HTGS_DRAFT;
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                                                                                                                                                                                                                                                                                                                                                                            ; Score 43.8; D; Pred. No. 0.31
0; Mismatches
                         Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                            459
                                                                               HTGS_FULLTOP; HTGS_ACTIVEFIN
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                                                                                                                                                                                                                                                                                                                                                                                                         210476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse
                          Euteleostomi;
; Murinae; Mus
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C57BL/6J,
                                                                                                                                   HTG 18-JAN-2002
C57BL/6J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                             0,
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TITLE

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ACCESSION
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TITLE
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                          38555 TAAAGAAAATGATGCCACAACCTACCCACATCTATGGGACAACATGAAAGCATTTCTACG
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                                                                                                                                                                                                                                                  429 tttcaaacaaggaaaattaattctcaaacca 459
                                                                                                                                                                                                                                                                                                                                      ctggaaattcatagctcacacttttttttaatggaagcaagagttggcaaacacactgcat 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                    tgaacaccatgatgatgctatcaggcctgatggagggagcaaccatgcaccttttcccct 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84;
                       Arabidopsis thaliana genomic AB008264 BA000015
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On Jan 15, 2002 this sequence version replaced gi:15208553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith, D.R.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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AB008264.1 GI:2618599
                                                                            AB008264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be preserved
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ilarity 55.6%;
Conservative
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clone_end:Sp6"
1 43240 c 44470 g 67886 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 225726: contig of 225726 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP23-101G12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: N/A
Chemistry: Dye-terminator Big Dye; 100% of re
Assembly program: Phrap; version 990315
Consensus quality: 225213 bases at least Q40
Consensus quality: 225480 bases at least Q20
Consensus quality: 22554 bases at least Q20
Insert size: 225825; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: gtc-seqcenter@genomecorp.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Genome Therapeutics Corperation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.genomecorp.com/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: GTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43.8; DB Pred. No. 0.31; 0; Mismatches
                                                                            79976
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                                                  chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
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                                                                         linear
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                                               P1 clone:MBD2
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990315
                                                                         PLN 27-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel:81-438-52-3935, Fax:81-438-52-3934)

Address for correspondence: kaos@kazusa.or.jp

For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cqi-bin/agd_graph.cqi?c=MBD2

Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi). Genes encoding tRNAs are predicted by tRNAscan-SE Genes encoding tRNAs are predicted by tRNAscan-SE Genes encoding tRNAs are predicted by tRNAscan-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MJB21 and the 3' clone is MRD20.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-OCT-1997) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structural analysis of Arabidopsis thaliana chromosome Sequence features of the regions of 1,191,918 bp covere seventeen physically assigned Pl clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 4 (6), 401-414 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakamura,Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1. .218)
/note="CDS is reported
gene_id:MJB21.20"
                                                                                                                                                /translation="MDSSSSVKIVSKSFVKPKTLPEESKQPYYLSPWDYAMLSVQYIQ
KGLLFHKPPLDSIDTLLEKLKDSLAVTLVHFYPLAGRLSSLTTEKPKSYSVFVDCNDS
PGAGFIYATSDLCIKDIVGAKYVPSIVQSFFDHHKAVNHDGHTMSLLSVQVTELVDGI
                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
/product="U2 snRNP auxiliary
join(5306. .5761,5932. .6828)
/note="gene_id:MBD2.2"
                       GLGKGYTLRSGYAHKFDGKVSAYPGREGGGSIDLEVCLVPEFMEALESDEEFMSLVSI
                                                  FAALKVHQAVAEHTSEKVSQMIDQWLKSPYIYHIDRLFEPMSVMMGSSPRFNKYGCEF
                                                                            RCITRARRLPLDRETSCRVAADNRGRMYPPLHKDYFGNCLSALRTAAKAGELLENDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Mitsui Pl"
                                                                                                 SLPYSHPDEFIRTYESPILKERMFCFSSETIRMLKTRVNQICGTTSISSFQSLTAVIW
                                                                                                                              {	t FIGLSMNHAMGDGTAFWKFFTAWSEIFQGQESNQNDDLCLKNPPVLKRYIPEGYGPLF}
                                                                                                                                                                                                                          /protein_id="BAB09184.1"
/db_xref="GI:9758571"
                                                                                                                                                                                                                                                                               protein"
                                                                                                                                                                                                                                                                                                      /product="N-hydroxycinnamoyl/benzoyltransferase-like
                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis
                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="MBD2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sato, S., Kaneko, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (strain:Columbia) DNA, clone_lib:Mitsui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acc# AB007647
                                                                                                                                                                                                                                                                                                                                                                                                                                     factor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       small subunit"
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bp covered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRAYVLGKLYQPKFYKRIVCLINFEHKKLSKHIPITNNCTVTS1"
complement()0in(14641. 14694,14770. .14868,18144. .15272,
15358. .15401,15497. .15569,15650. .15736,15848. .15932,
16050. .16133,16204. .16733,16863. .17553,17677. .18603))
/note="gb|AAF23287.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RETNPKSWFYTCKDCGVTFHIFCVVWDIRFSKQGETIRDGVELLPNNTSSRPLCKNCQ
CRCLGPFFVKDYDNICYCSYYCYARLHSLRYIWSKFRCPPWISEPST"
COMPLEMENT (join (1094. .11250,11343. .11490))
                                                                                                                                                                                      LGSADQADMGSIGTSQEGSSTGSPVQDENKITIKDMHISAGDFEKSQSASGESILQPE
IEEEQFFSDLDECKFGGNSSYGSSSSDTYKVDGKESYDETKTSPEKGYENTMALSEP
INIEEKKDIFTDEMERLYGGIPIMKIQNUDDMDASPSQPLSQSFDDFCNTSKLDLEED
ESSSGGLDAESVAESSPKLKAFKHVIANPEVVELSLCKHLLSEGMGAEAASQAFNSEK
LDMEKFASLGPSILENDKLVVKIGGCYFDEDAAAFILLGVVSFGTAQVFEFKGMIAVD
RNEKFGGDVLAOGSGSMKLWEPFSLRSTKEAEASPSGDTAEPEEKQEKSESPTBMKTVR
ALTPTSEQLASLDLKDGMNSVTFTFSTNIVGTQQVDARIYLMKWNSRIVVSDVDGTIT
                                                                                                                                                                                                                                                                                                                                                                                                                 RSVRESQDCGVERAEIAADLLEVKWSTNIDTRKRGKGMSSESLDGKDYGESTSTSGKS
CVEGSSEMLVDSDSILETPLVASPTLRFLDEKEQDFRESTNVEDYCEEDGSSGVVVEN
GLCEASSMVFSVTSEGSGNVEIFVEPRTEALAEDAVSGSDLDSKQELLRAPESVEIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mnavgrigsyiyrgvgtvsgpfhpfggaidiivveqpdgtfkss
pwyvrfgkfqgvlkngrnliridvngvdsgfnmylahtgqayflrevedvvgesesge
vytlssgdeaettsrddvvdkvkiplksrscnydspsprtgngkivgkpgilgyvfgg
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strong similarity to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FHSTPVLTSPMGSPPHSHSSSSRFSKINGSKRKGHAGEKQFAMIEEEGLLDDGDREQE
ALPRRCYVLAFIVGFSLLFAFFSLILYAAAKPQPKJSVSSTEEQLKYQAGQDAGGI
GTDMITMMATLRMLYKANGTFEGVHYTSSPIDLSESQITIGGGSIKKTYQSKRKSQRTV
VVNVLGDKIFLYGSGSTLVPPPPPPAPIPKPKKKKGPIVIVEPPAPPAPVPMRLNFTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MTLKKVDANPSTLESSLQELKSDETSRSKINFILFLADNDPTTG
QSWCPDCVRAEPVIYKTLEEFPEEVKLIRAYAGDRPTWRTPAHPWRVDSRFKLTGVPT
LVRWDGDSVKCRLEDHQAHLPHLILPLLAPST"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(12261. .12611,13086. .13271,13354. .13779))
/note="emb|CAB53482.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/protein_id="BAB09186.1"
/db_xref="GI:9758573"
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GIVQKEYAIGCTKCNYFLDFRCATLPLTVRLPRYDDHPLTLCYGDEKASGKCWCDICE
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VCP1GTDTFYNCSESSCSFVLHETCAN1SKKKRHFLSPVPLVLCLQNQRNTETCNACQ
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CAKLPRVIHVNHHDHRVSYKYPLGPGEWRCGVCWEEIDWSYGAYSCSLCPNYAMHSLC
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CASVFDSPEITHPSHVRHPLKLRSNGAPDYTNLNCHICGDATGNLLYHCDICKFNLNM
                                                                  DENTWNFWKLPPPSLM"
                                                                                                                              RSDVLGQFMPLVGIDWSQTGVTHLFSAVKENGYQLIFLSARAISQASVTRQFLVNLKQ
DGKALPDGPVVISPDGLFPSLFREVIRRAPHEFKIACLEEIRGLFPPEHNPFYAGFGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/protein_id="BAB09188.1"
/db_xref="GI:9758575"
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/protein_id="BAB09187.1"
/db_xref="GI:9758574"
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/protein_id="BAB09185.1"
/db_xref="GI:9758572"
                                                                                                RDTDEISYLKVGIPRGKIFIINPKGEVAVNRRIDTRSYTNLHTLVNRMFPATSSSEPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MHAKTDSEVTSLSASSPTRSPRRPAYFVQSPSRDSHDGEKTATS/
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                           40974 ATAGACAACTATTTAAAAGATACAAACATAAAATTTCTAGTCGTAATTTTATGTTTAATT 41033
                                                                                                                                                                                                                                                                                                                                                                                                                                             40914 ATTTAAATTCTAGAGAATTTGAGGTTATTGTCTCTAAAAATTTTAAATATTTTAGCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427 attitcaaacaaggaaaattaattctcaaaccatcatgacatgcaattctcaaaccatgc 486
667 cacgaaaatgc
                                                                                                                                                                                                           TAGAGGCAAAAAGGTAAGAGAATTTAATCTTTTTATAAATTGATTTTTAGGAAAGACAAT 41093
                                                                                                                                                                                                                                             accgacgagtccatgcgaggtggaaacgaagaactgaaaatcaacatcccagttgtcgag 546
                                                                                         ATATAAATTGAACTAAATATAAAGTTTTTTGGTCTATCATTGATTTGAGTATTATTATTG 41153
                                                                                                                                           Conservative
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KGSLSAAQKFTPDIFFKSKL"
complement(join(25760. .25834,27425. .27528,27615. .27900,
27989. .28171,28527. .28634))
/note="gene_id:MBD2.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSESSSTDQESVGTEMEKETDQESVAIEHLQKQ"
complement(30319 . 31245)
/note="gene_1d:MBD2:10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(23380. .23461,24198.
24707. .24832))
/note="gene_id:MBD2.8
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NREMSVRKAELKEANGKAEKARDGKLGMEQELRKWRSENGKRRTDEGREPEKSPTRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAEEKRFSVAMARDQDVYNWEKELKMVENDIERLNQEVRAADDVKAKLETASALQHDL
KTELAAFTDISSGNLLLEKNDIHAAVESARRELEEVKANIEKAASEVKKLKIIAGSLQ
SELGRERQDLEETKQKESTGLARTNDKDAGEELVETAKKLEQATKEAEDAKALATASR
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RAFVYPRSVESPRFGSPRSVESPCFGSPIGVIDTASPFESVREAVSKFGGITDWKAHK
IQTIERRKMVDEELEKIQEAMPEYKREAELAEEAKYDALEELENTKGLIEELKLELEK
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/protein_id="BAB09189.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGFWQKINVKQPEHRINGRHGGNSHEFLRSPWIKHYKPLVKTQIPVTDEPENQVVSSS
NGKKGICSSGSASSLKQLSSHSRDHDQISVGEEVSDQNFVNEGIKGENGSSKKMKTVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence-not_experimental
/protein_id="BAB09191.1"
/db_xref="G1:9758578"
/translation="MVGDYRGRFSSRRFSDDSDDSSDDASSVEGETTSSMYSAGKEYM
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/protein_id="BAB09190.1"
/db_xref="GI:9758577"
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IEMVSNEYKDMLREKELAAERADIAVLEAKEIERTMDGLSIELIATKELLESVHTAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="non-LTR retroelement reverse transcriptase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETEWTNEKHSLYLKSMEASFVDQLYNSLGALGKNENVSESTRFGSGRKPSQEQFKVLH
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/translation="MLGDDKDSDDLNLFLNAIGEAGDEEGPTSFNDIDFLTFDDEDLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41.4; DI
Pred. No. 1.3;
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University, 4444 Forest
4 (bases 1 to 96217)
                                                                                                                                                                                                                                                                                             Submitted (11-AUG-1997) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 3 (bases 1 to 96217)
                                                                                                                             Submitted (04-FEB-2000) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis,
                                                                                                                                                                                    Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Graves, T., Hinds, K., Sutterer, C. and Biewald, T. The sequence of H. sapiens BAC clone CTA-264L19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center project name: H_RG264L19
                                      Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                                                                                Genome Center
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Project and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send an E-mail to egreen@nhgri.nih.gov The sequence of this clone was established as part of a mapping sequencing collaboration between the NHGRI Chromosome 7 Mapping and

SOURCE INFORMATION:

This clone is from a release of the human BAC library. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).
VECTOR: pBeloBAC11

Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the left is CTB-13P7, 200 bp overlap. The

actual start of this clone is at base position 63963 of CTB-13P7; actual end is at 96217 of CTA-264L19. This clone is part of an unanchored island, orientation is unknown.

FEATURES repeat_region source repeat_region repeat_region repeat_region This clone contains STS sWSS2954 (NID:g1113657). /rpt_family="ALU"
complement(79278.
/rpt_family="L1" /rpt_1 67429. /rpt_1 /rpt_ 45804 /rpt_1 43696. /rpt_family="ALU" complement(23151. /rpt_family="L1" 6589 /rpt_tamil 80325. .80 /rpt_family="L1" /rpt_family="MER" complement(44468. /rpt_family="ALU" 41105. .41394 complement(31054.
/rpt_family="L1" /rpt_family="ALU" complement(28673. /rpt_family="L1" /rpt_ 22657 complement(11846. /rpt_family="L1" complement(85475 complement (73310 complement (54849 complement(39149 complement (33330. /rpt_family="L1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:,
                                                                                                                                                                                                                                                                                                                                       On May 20, 2001 this sequence version replaced gi:13274323. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Human DNA sequence from clone RP11-48719 on chromosome X, complete
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Similarity 47.5%;
22; Conservative
                                                   database can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence. The true right end of clone RPI1-274M8 is at 100 in sequence.
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                                                                                                                 /note="AluSx repeat: matches 1. 17611. .17646
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/note="MIR repeat: matches 1. .199 of consensus" 18160. .18382
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9102. .9441
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                                     /note="AluSg repeat:
17945. .18142
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                                                                                                                                                                                                                                                                                                                                                         /note="MER53 repeat: matches 1.
14038. .14282
                                                                                                                                                                                                                                                                                                                                                             14038.
                                                                                                                                                                                                                                                                                                                                                                                                     13800.
                                                                                                                                                                                                                                                                                                                                                                                                                                            11810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9445. .9971
/note="Tigger3b repeat: matches 2. .540 of consensus"
9974. .10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Tigger3b repeat: matches 887. .1231 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluSp repeat: matches 1.
2450. .2552
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/db_xref="taxon:9606"
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                                                                                                 /note="MIR repeat: matches 199.
                                                                                                                                                                           note="MIR repeat: matches 84.
                                                                                                                                                                                                                   /note="MER20 repeat: matches
                                                                                                                                                                                                                                                        note="AluSq/x repeat: matches 1. .111 of consensus"
                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 10.
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MIR repeat: matches 23.
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                                                                                                                                                                                                                                                                                                 repeat: matches 6105. .6169 of consensus"
                                                         matches 2.
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                                                                                                                                                                                                                                                             /note="9 copies 4 mer gtgt 91% conserved"
35365. 35535
/note="MER45 repeat: matches 1. .171 of consensus"
36270. 36567
/note="AlluSp repeat: matches 1. .298 of consensus"
41820. .46785
/note="11PA6 repeat: matches 11. .4967 of consensus"
46786. .47086
/note="41UY repeat: matches 3. .299 of consensus"
/note="11PA6 repeat: matches 3. .299 of consensus"
/note="11PA6 repeat: matches 4967. .6141 of consensus"
48774. .48803
                                                 51509. .51638
/note="FLAM_A repeat:
51679. .51898
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/note="L1MA9 re
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20458. .20
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                                                                                                                                                                                           /note="LiM4c repeat: matches 905. .934 of 49784 .49831 /note="12 copies 4 mer caca 93% conserved" 49863 .50116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSq repeat: matches 247. .300 of consensus" 31157. .31458
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                                                                                     /note="MER44 repeat: matches 421. .728 of 51509. .51638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 30. .262 of consensus" 18803. .19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33312. 3344A
/note="FLAM_A repeat: matches 1.
34016. 34172
/note="MER5A repeat: matches 32.
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23112. .23183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MLTIC repeat: matches 131. .466 of 20768. .20931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19470. .19565
/note="AluSg/x repeat: matches 212. .307 of consensus"
19571. .19723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSg repeat: matches 1.
19223. .19345
                                  /note="MER58B repeat: matches
                                                                                                                                                                         /note="AluSx repeat: matches 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 31. .261 of consensus"
29016. .29069
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.20767
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                                                                     matches
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                                                                     <u>-</u>
                                  114. .341 of consensus
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Matches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ataaatgtttttgtaaacaaaataaatactta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATTTCTTTCTTTTTTTTTTAGCATATGACATTTTTAGTCTGTAGGTCTTATTTAGTG 12437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tcatttacatacatgtacaaatacataatgtaccctacaatttgttttttggagcagagt 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atgatcggtcggagacgacggacaatcagacactcaccaactgcttttgtctgggacaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggtgtggtctttttttttttacacgaaaatgccatagctggcccgcatgcgtgcagatcgg 706
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105; Conserv
                                      Dodge, S., Dominu, M., Ginde, S., Goyette, M., Granam, L.,
Galagan, J., Gardyna, S., Ginde, S., Heaford, A., Horton, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, C., Mlenga, V., Morrow, J.,
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
McCarthy, M., McCarthy, M., McCarthy, Morrow, J.,
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
McCarthy, M., McCarthy, M., McCarthy, Miranda, C., Mlenga, V., Morrow, J.,
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
McCarthy, M., McCarthy, M., McCarthy, Miranda, C., Menga, V., Morrow, J.,
McCarthy, M., McCarthy, M., McCarthy, Miranda, C., Mlenga, V., Morrow, J.,
McCarthy, M., McCarthy, M., McCarthy, Miranda, M., McCarthy, Miranda, M., McCarthy, Miranda, M., McCarthy, M., McCarthy, M., McCarthy, Miranda, M., McCarthy, M., McCarthy, Miranda, M., McCarthy, M., McCar
                                                                                                                                                                                                                                                                                                                                                                                             Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Callins,S., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Colloge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Castle,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Colloge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Callins,S., Colloge,S., Colloge,S
Murphy,T., Naylor,J., Norman,C.H.,
O'Neil,D., Olivar,T.M., Oliver,J.,
Pisani,C., Pollara,V., Raymond,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142184 bp DNA linear i
Homo sapiens chromosome 12 clone RP11-631A22 map 12,
SEQUENCE, 18 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 12, clone RP11-631A22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Cn
Mammalia; Eutheria; Pr
1 (bases 1 to 142184)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC037428.2 GI:8077012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 142184)
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59121. .59259
/note="MER33 repeat: matches 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="20 copies 2 mer tg 90% conserved" 58373. .58500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55248. .55774
/note="LTR40a repeat: matches 8.
57036. .57339
/note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1MA8 repeat: matches 5986, .6242 of consensus"
57912, .58211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54482.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58373. .58500
/note="L2 repeat: matches 1651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1ME2 repeat: matches 6011. .6145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="AluSx repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metazoa; Chordata;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .54616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .59004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 58259
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Pred. No. 2.2;
0; Mismatches 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                798
                                 Peterson, K., Pierre, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1778 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .294 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .149 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .295 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 133021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .517 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consensus "
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WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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COMMENT

JOURNAL

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Roy.A., Santos,R., Schauer.S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (08-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced gi:7528141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.
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Consensus quality: 134528 bases at least Q40
Consensus quality: 138011 bases at least Q30
Consensus quality: 139354 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 140484; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; sum-of-contigs
Quality coverage: 5.2 in Q20 bases; sum-of-contigs
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Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
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6425 8723: contig of 2299 bp
8724 8823: gap of 100 bp
8824 12084: contig of 3261 bp
12085 12184: gap of 100 bp
12185 17926: contig of 5742 bp
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1395 1494: gap of 100 bp
1495 2814: contig of 1320 bp in length
2815 2914: gap of 100 bp
2915 4040: contig of 1126 bp in length
4041 4140: gap of 100 bp
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100776: contig of 13481 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
On Jun 29, 2000 this sequence version replaced gi:6451951.
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=K1787
Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.orni.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://ccr.081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.iastate.edu/gi-bin/sp.cgi).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, http://genome.wustl.edu/eddy/tRNAscan-SE/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thaliana chromosome 3. II. Stequence features of the 4,251,695 bp regions covered by 90 Pl, TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is T26612 and the 3' clone is T20F20.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-NOV-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaneko,T.,\ Kato,T.,\ Sato,S.,\ Nakamura,Y.,\ Asamizu,E.\ and\ Tabata, Direct\ Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
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Res. 7 (3), 217-221 (2000)
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                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                             .81580
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                                                                                                                                             complement(35843.
                                                                                                                                                                           PVPSQSSRNSVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown protein"
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                                                                                                                                                                                                                                                                                                          LRLVLFPRRDLFVGEEKPSLICDVFAGNHDFHAVSSQLSHKFVREIFVTKFATEYRLG
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to non-LTR retroelement reverse
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Best Local
                                                                      42666 TCTCAAACTAGTTAGCTATAAGTTTTTTTTAATAAAAAACCGAATCAAAACTCAAATCGA 42607
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tttcaaacaaggaaaattaattctcaaaccaccatgacatgcaattctcaaaccatgca 487
                                                                                              tctggaaattcatagctcacacttttttttaatggaagcaagagttggcaaacacatgca 427
                                                                                                                                                                  88;
                                                                                                                                                                                       Similarity
                                                                                                                                                                  Conservative
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LLQCTQHMCPIRVHWHVKTSYKEYWRVKVAITNENYNMNYSQWNLVVQHPNFDNLTKL
FSFNYKPLNPYLNINDTAMLWGIKFYNDFLSQAGPVGNVQSELLFQKNPLEFTFEKGW
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                                                                                                                                                                                                                                                                               DEPTYSPKEAGDILSHLLNDLRSSRTLTVCSYLLEVISECNDPVDMLRDVQAQHLVLE
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.id:K17E7.10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named tindicate the level of evidence for their annotation. Genes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GenemarkHMM (Mark Borodovsky,
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Town, C.D. and Kaul, S.
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/gene="F21N10.12"
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/chromosome="1"
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/cultivar="Columbia"
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4.1%; Score 40.6; DB 8; Length 98017; larity 52.7%; Pred. No. 2.4; Conservative 0; Mismatches 79; Indels 0; Gaps	Query Match Best Local Similar Matches 88; Cor	/rpt_family="ARNOLD2 ARNOLD2 Autonomous DNA-transposon ARNOLD2." 88308913	epeat.
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<pre>/rpt_family="ARNOLD4 ARNOLD4 Autonomous DNA-transposon ARNOLD4." 95259634</pre>	repeat_region	13685694 /rpt_family="ATCOPIA161 ATCOPIA161 Internal region of ATCOPIA16 copia-like LTR-retrotransposon."	repeat_region

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.y="arNOLD3|arNOLD3 Autonomous DNA-transposon
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                                                                                        Score 40.6; DB 8; Length 98017; Pred. No. 2.4; 0; Mismatches 79; Indels 0;
                                                                                          0; Gaps
                                                                                            0;
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REFERENCE
AUTHORS
TITLE
                                                          RESULT 12
AP003681/c
LOCUS
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REFERENCE
AUTHORS
TITLE
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AUTHORS
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SOURCE
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AC074329/c
            ACCESSION
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Best Local Similarity
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                                                                                                                   CTTGACAATATACCTAAAAGCTCTAGAACAA 107159
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                                                                                                                                         tttcaaacaaggaaaattaattctcaaacca 459
                                                                                                                                                                  AGGAAAACTCATAGCTCAGAGAGTCTTCAAAAAAGAAACTAGAGAAAGCACACACTAGCAG
AP003681
AP003681.2
HTG.
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Street, Waltham, MA 02453,
3 (bases 1 to 207872)
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P
                                                                                                                                                                                                                                                                                                                                                                                                                                               Street, Waltham, MA 02453, USA
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG
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Mus musculus chromosome 12 clone
                                              Oryza sativa genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Data
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                   complete sequence.
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                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               1, 2001 this sequence version replaced gi:9885988
Location/Qualifiers
1. 207872
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/clone_lib="RPCI-23"
40080 c 40327 g 63334
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/chromosome="12"
             GI:18652929
                                                                                                                                                                                                                                                                       4.1%;
54.3%;
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                                                                                                                                                                                                                                                                      Score 40.6;
Pred. No. 2.
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53, USA
                                                          65955 bp
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                                               chromosome
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RP23-257D2
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me 1,
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2 strain
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                                               clone:81158C05
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C57BL/6J,
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                                                          PLN 13-FEB-2002
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ORGANISM
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TITLE
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51328 CGCCTGTGCCCGAAACAGAAGGCCATGTCGGAATCGTAAACCCCTGGATGTGACATATTCT 5126
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nes 121; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTCGGACACGAAGAACTAACCTAAAGCCGTCCATGGCTTCCATGCCTCTACCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CT--AATTACATAGATTGGTTTTTTATCGGACGGAGGGAGTACATACCACACACTTGCAT 51151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctggaaattcatagctcacacttttttttaatggaagcaagagttggcaaacacatgcat 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTATACAATGAATATAGATAGAGGTATGTCCAAATTCGTAATACTAGAATATGTCATAT 51209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgaacaccatgatgatgctatcaggcctgatggagggagcaaccatgcaccttttcccct 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFMAL13P3 318221 bp L
Plasmodium falciparum chromosome 13
PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobiological Sciences, Rice Genome Research Program; 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (cultivar:Nipponbare) DNA,
Oryza sativa
                     on Aug 24, 1999 this sequence version replaced gi:5731882. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: Th sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Feb 12, 2002 this sequence version replaced The orientation of the sequence is from M13rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                Direct Submission Submitted (15-MAR-1999) P.falciparum Genome Sequencing Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                            malaria parasite P. falciparum
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                                                                                                                                                                                                                                                                                and Barrell, B.
                                                                                                                                                                                                                                                                                                          Bowman, S., Churcher, C.,
                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum
Eukaryota; Alveolata;
                                                                                                                                                                              CB10 1SA, UK
                                                                                                                                                                                                      The Sanger Centre, Wellcome Trust Genome Campus,
                                                                                                                                                                                                                                                                                                                                  (bases 1 to 318221)
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/chromosome="1"
/clone="B1158C05"
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/cultivar="Nipponbare"
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50.8%;
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change as work continues.
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Pred. No. 3.3;
0; Mismatches 115;
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                                                                                                                                                                                                                                                                                                          Harris, B.,
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3D7, ***
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to -21M13 of the BAC
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SEQUENCING IN
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JOURNAL
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TITLE
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tggagcagagtggtgtggtcttttttttttacacgaaaat
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l (bases 1 to 7218)

Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.

Recombinant fowlpox virus

Patent: US 5670367-A 14 23-SEP-1997;

Location/Qualifiers
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Order of segments is not known; 800 n's separate segments
NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                              Unclassified
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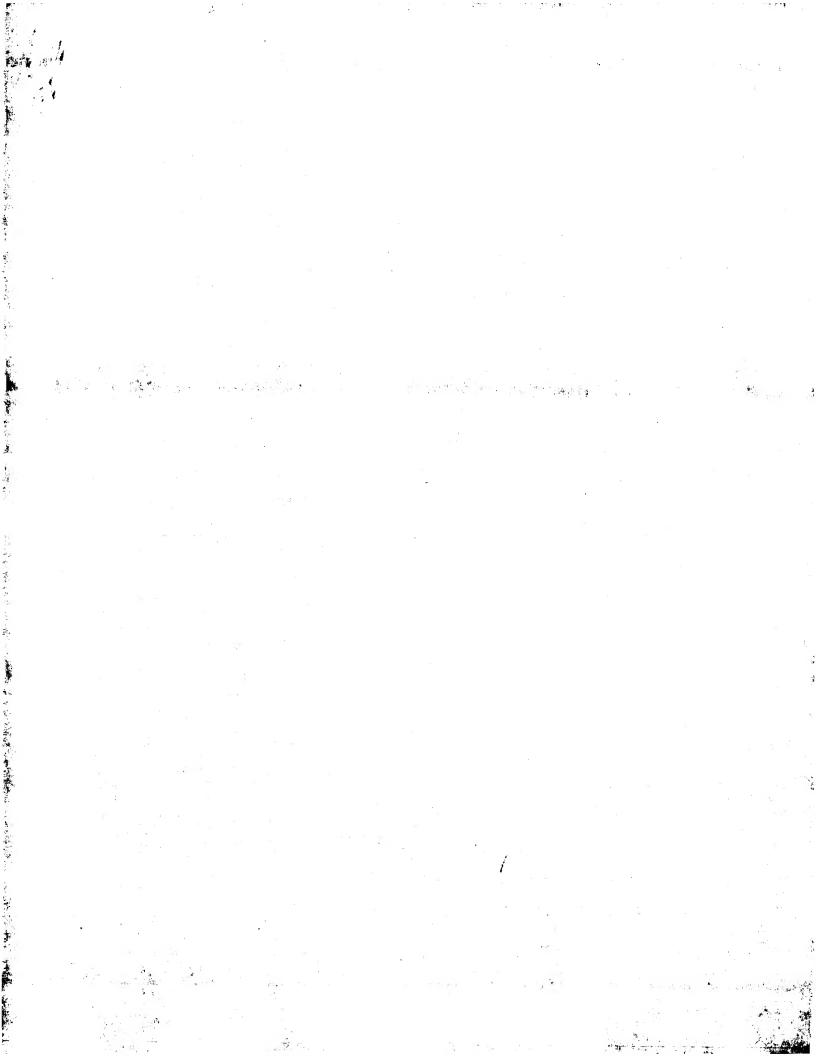
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Location/Qualifiers
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tive 122; Mismatches
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ALIGNMENTS

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RESULT
AAX34650
Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; G; starch branching enzyme; starch soluble synthase; debranching enzyme endosperm; wheat; barley; granule-bound synthase; glutenin; starch; grain softness protein I; bacterial isoamylase; glycogen synthase; wSBE I-D4 gene; ss.
         (CSIR ) COMMONWEALTH SCI & IND RES ORG (GOOD-) GOODMAN FIELDER LTD. (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD. (AUSU ) UNIV AUSTRALIAN NAT.
                                                                      20-MAR-1998;
12-SEP-1997;
                                                                                                         11-SEP-1998;
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                                                                                                                                                                                 Triticum tauschii.
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97AU-0009108
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Best Local Similarity 100.0%;
Matches 1000; Conservative
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                                                              The present sequence encodes a wheat starch branching enzyme of Aegilops tauschii, designated F2. A. tauschii is likely to be the ancestral D genome donor of wheat. Probes isolated from the present sequence were used to identify type II starch branching enzymes (SBI in wheat, especially BEIIb. The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose
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(GOOD-)
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and amylopectin content of cereal pla
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ABL34155/c
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                                                                    Query Match
Best Local
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7849
                                                                                                                                                  macular degeneration, arteriosclerosis, anaemia, cancer, acute mys Leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                       genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                              The present invention provides a number of human immune system associated
                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chen for diagnosis and treatment of diseases
                                                                                                                                                                                                                                                                                                                                                            WPI;
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01-SEP-2000;
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01-AUG-1995;
12-JAN-1996;
14-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This cDNA clone codes for quail VEGF-C (AAW00934), a novel ligand that binds specifically to the Fit4 receptor tyrosine kinase (VEGFR-3), stimulating phosphorylation of the receptor. The clone was isolated from a quail cDNA library using mouse (see AAR84277) and human (see AAR84276) VEGF-C cDNA fragments as probes. The isolated polynucleotide can be used to produce recombinant polynopeptides corresponding to non-human mammalian variants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flt4 receptor tyrosine kinase ligand and related nucleic acid to modulate growth of endothelial cells and for diagnosis of endothelial cell diseases  \begin{array}{c} \text{ } \\ \text{ } \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-145688/13.
P-PSDB; AAW00934.
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vascular endothelial growth factor receptor-3; ligand;
angiogenesis; wound healing; lymph vessel; therapy; diagnosis; ss.
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55.7%;
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                                                                                          activities affecting growth and migration of vascular endothelial cells, promoting growth of lymphatic endothelial cells and lymphatic vessels, increasing vascular permeability, and affecting myelopoiesis. The products can be used for stimulating angiogeneses, for inhibiting angiogenesis, for stimulating lymphangiogenesis, treatment or prevention of inflammation, oedema, elephantiasis, or Milroy's disease. They can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
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                                                   also be used to modulate myelopoiesis, e.g. treating granulocytopenia. They can also be used for modulating the growth of endothelial cells. They can also be used to stimulate lymphocyte production and maturation
                                                                                                                                                                                                                                                New isolated vascular endothelial growth factor polypeptide(s) - used to develop products for treating, e.g. cancers, inflammation, oedema, granulocytopenia or for wound healing or tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV52578 standard; cDNA; 1741 BP
Sequence
                                                                                                                                                               The vascular endothelial growth factor C (VEGF-C) polypeptides have activities affecting growth and migration of vascular endothelial cells,
                                                                                                                                                                                                           Example 20; Page 121-123; 177pp; English.
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445 A;
                           inhibit trafficking of leucocytes between tissues and or to affect migration in and out of the thymus.
455 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                    macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzhelmer, s disease, ALDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                          The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising for diagnosis and treatm
                                                                                                              Sequence
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01-SEP-2000;
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    Score 35.2; D
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0; Mismatches
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0; Mismatches
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bowel disease;
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l Similarity 85; Conserv

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Indels Length

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Score 34.6; DI Pred. No. 2.4; 0; Mismatches

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710;

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RESULT 8
AAI97878/c
                                6
                                                gene
                                                            The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy susceptibility indicators or tumour markers for anti-cancer agents. The susceptibility indicators or tumour markers for anti-cancer agents. The susceptibility indicators or tumour markers for anti-cancer agents.
                                                                                                                                                                               neuroblastoma, malignancy
for anti-cancer agents -
                                                                                                                                                                                           Nucleic acids originating in gene expressed in human neuroblastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour managements.
                                                                                                                                                                                                                                                                WPI;
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                                for N-myc
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BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JAN-2001;
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2000US-0214886
2000US-021647
2000US-0216880
2000US-0216880
2000US-0217496
2000US-0218290
2000US-022964
2000US-022964
2000US-0229521
3000US-0225213
2000US-0225266
2000US-0225266
2000US-0225277
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2000US-0190076.
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2000US-0232397
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2000US-0232401
2000US-0233063
2000US-02334997
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2000US-0235834
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                                                                                                                                                                     The invention relates to novel genes (AAL34669-AAL37666) and proteins C (ABB03087-ABB04109) associated with the musculoskeletal system useful CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC protein or gene therapy. The genes are isolated from a range of human CC tissues disclosed in the specification. The nucleic acids, proteins, CC antibodies and (ant)agonists are useful in the diagnosis, treatment CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and CC other cancers of the adrenal gland, bone, bone marrow, breast, CC gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis, CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound CC and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                          Query Match
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                                                                                                                                                                                             parasitic infections.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                Sequence 32220 BP; 9865 A; 6658 C; 6011 G; 9685 T; 1 other;
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 464 gacatgcaattctcaaaccatgcaccgacgagtccatgcgaggtggaaacgaagaactga
                                       850
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                                                 2001-451937/48.
                                 CA,
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2000US-0249265
2000US-0249297
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2000US-0251856
2000US-0251869
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2000US-0249217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO 3933;
                                                                                                         3.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    781pp + Sequence Listing; English
                                                                                          Score 34.6; D
Pred. No. 23;
0; Mismatches
                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MS
                                                                                                                        DΒ
                                                                                           84;
                                                                                                                      22;
                                                                                           Indels
                                                                                                                     Length 32220;
                                                                                          0;
                                                                                        Gaps
                                  791
                                                             463
                                                                                          0;
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RESULT 1

ADAKS7698

ID AKS7698

ID AKS7698

AX AKS

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18-AUG-2000
22-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
30-AUG-2000
01-SEP-2000
01-SEP-2000
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05-SEP-2000
05-SEP-2000
06-SEP-2000
06-SEP-2000
                                                                                                                                                                                                                                                                                               26-JUL-2000
14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK57698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK57698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aaatcaacatcccagttgtcgagtcgagaagaggatgacactgaaagta 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAATAATATTACAATAGGACTTTGAGTGTGCATTTCACAGTGGAAATA 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTTCTCATACTCTAGCCCTGACCTTGCAGTCTCCTCTGAGGGGCCTCCTAAGACCCTT 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune/haematopoietic antigen encoding cDNA SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; cDNA; 362
2000US-0226279.
2000US-0226681.
2000US-0226868.
2000US-0227182.
2000US-0227182.
2000US-02298924.
2000US-0229343.
2000US-0229344.
2000US-0229345.
2000US-0229345.
2000US-0229345.
2000US-0229343.
2000US-0229345.
2000US-0229345.
2000US-0229343.
                                                                                                                                                                                                                                                                                               2000US-0214886.

2000US-0215647.

2000US-0216880.

2000US-0217487.

2000US-0217496.

2000US-0218290.

2000US-022964.

2000US-0224518.

2000US-0224518.

2000US-0224519.

2000US-0225266.

2000US-0225266.

2000US-0225267.

2000US-0225267.

2000US-0225267.

2000US-0225267.

2000US-0225267.
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2000US-0205515.
2000US-0209467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0189874
2000US-0190076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US01354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IJ
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RESULT 11
ABL33293/c
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Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
11-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis an treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the protein acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, associated diseases, especially associated acids account of the protein and polynucleotides may be used to prevent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen useful for preventing, diagnosing and/or treating cancers metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                  cancers and cancer metastases of haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the avamentification.
                ABL33293
                                                ABL33293 standard; DNA; 9725
                                                                                                                                                                                                                                                                                                                                                                 Sequence 362 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                  represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                        303
                                                                                                                                                                                                         243
                                                                                                                                                        catggccaggtaaacgcgctcccagccgttggtttgcgatctcgtcct 875
                                                                                                                              aagatcaaggtgccagcacggtcagtttttggtaagggctctctttct
                                                                                                                                                                                                                         taaatgtttttgtaaacaaataaataacttataaacgagggtactagaggccgctaacgg 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-483426/52.
DB; AAM84917.
                                                                                                                                                                                                         tatatgttttttttaacttaacataaatttattttcacagttctagaggctagaaatcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2758; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0249245.
2000US-0249264.
2000US-0249297.
2000US-0249297.
2000US-0249390.
2000US-0250160.
2000US-0251030.
2000US-0251988.
2000US-0251988.
2000US-0251868.
2000US-0251868.
2000US-0251869.
2000US-0251869.
2000US-0251869.
2000US-0251989.
2000US-0251989.
2000US-0251989.
2000US-0251989.
2000US-0251989.
2000US-0251989.
                                                                                                                                                                                                                                                                          3.4%;
ilarity 57.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                 89
                                                                                                                                                                                                                                                                                                                                                               A; 80 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben
                                                                                                                                                                                                                                                                        ; Score 34.4; DB; Pred. No. 1.9; 0; Mismatches
                                                ВP
                                                                                                                                                                                                                                                                                                                                                                 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM;
                                                                                                                                                                                                                                                                                                                                                                 G; 106 T; 2 other;
                                                                                                                                                                                                                                                                                                              DВ
                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                             22; Length
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides, and
                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                          Gaps
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and

2000US-0231242 2000US-0231243 2000US-0231414 2000US-0231414 2000US-0232081 2000US-0232081 2000US-0232398 2000US-0232399 2000US-0232399 2000US-02333063 2000US-02333063 2000US-02333063 2000US-02334997 2000US-0234997 2000US-0234997 2000US-0235834 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-024678 2000US-024678 2000US-024678 2000US-0246611 2000US-0246613 2000US-0246613 2000US-0246523 2000US-0246523 2000US-0246523 2000US-0246613 2000US-0246613 2000US-0246523 2000US-0246523 2000US-0246523 2000US-0246613 2000US-0246523 2000US-0246613 2000US-0246523 2000US-0246523 2000US-0246523 2000US-0246613 2000US-0246523 2000US-0246213 2000US-0249213 2000US-0249213

25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 29-SEP-2000;

29-SEP-2000; 29-SEP-2000;

14-SEP-2000; 21-SEP-2000; 21-SEP-2000; 25-SEP-2000;

14-SEP-2000;

29-SEP-2000
22-CCT-2000
02-CCT-2000
03-NOV-2000
04-NOV-2000
06-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
09-NOV-2000
09-NOV-2000
09-NOV-2000
09-NOV-2000
09-NOV-2000
09-NOV-2000
01-NOV-2000
09-NOV-2000
01-NOV-2000

26-MAR-2002

entry)

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AAF24892
ID AAF:
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                                                                                                                                                                                                         Qγ
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Best Local
                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                   7136
                                                                                                                                                                                                                                     7196
                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of human immune system associat genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                AAF24892
                                                                              7016
                                                                                                                                7076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antirheumatic; antiarthritic; antidiabetic; antipsoriatic antiinflammatory; cancer; eye disease; arteriosclerosis; acute myeloid leukaemia; Alzheimer's disease; AIDS; epile neurofibromatosis; rheumatoid arthritis; psoriasis; bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                       Sequence 9725 BP; 2521 A; 335 C; 2382 G; 4487 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                         425
                                                                                                      485
                                                                                                                                                                                                           365
                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leic acid comprising fragment of chemically modified diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P
                                                                                                                                                                                                                                                           gcattttcaaacaaggaaaattaattctcaaaccaccatgacatgcaattctcaaaccat 484
                                                                                                                                                                                                                                    2002-130909/17
                                                                                                     gcaccgacgagtccat 500
                                                                                                                                                                                   ccctctggaaattcatagctcacactttttttttaatggaagcaagagttggcaaacacat 424
                                                                              GCAACCAAAATTAAAT
                                                                                                                                1;
                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPIGENOMICS AG
              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system associated
              DNA;
                                                                                                                                                                                                                                                                                                   3.4%;
48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ç
                20394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                   Score 34.4;
Pred. No. 13;
                ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ζ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID
                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO:
                                                                                                                                                                                                                                                                                       101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antipsoriatic;
                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune system associated rtosines. The sequences
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epilepsy;
bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene, us
                                                                                                                                                                                                                                                                                                               9725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anaemia;
                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                  7077
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RESULT 13
AAS61304/c
ID AAS61304 s
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a polyketide synthase which is associated with the biosynthesis of pimaricin. The polyketide synthase polypeptide is useful for the oxidative modification of a methyl group of a suitable compound, e.g. a bioactive compound including a secondary metabolite, antibiotics and anticancer agents. Recombinant cells comprising the gene are useful for the production of pimaricin. The polyketide synthase polynucleotide may be over expressed in Streptomyces, leading to an increase in the biosynthesis of pimaricin, as a source of primers for
AAS61304
                                                                                                                           7773
                                                                                                                                                                                                 7713
                                                                                                                                                                                                                                                                         7653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amplification reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides encoding enzymes involved in the biosynthesis pimaricin, useful for modifying the biosynthesis of pimaricin and the synthesis of new compounds \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polyketide synthase; oxidative modification; metabolite; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martin JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200077222-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF24892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (STAM)
                                                                                                                                                               964
                                                                                                                                                                                                                                     904
                                                                                                                         cgacttccacac
                                                                                                                                                               acacactcacac
                                                                                                                                                                                                                                                                   cgcgtccggccgccgcaccctgaccgcccgctccagggcggagggcgacggcgaccgccc 7712
                                                                                                                                                                                                                                                                                          cgctcccagccgttggtttgcgatctcgtcctccgccacgcagcgtcgcctccaccgtcc 903
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Similarity 53.8%;
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                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        7486 C;
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Pred. No. 20;
0; Mismatches
                                     ВP
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                                                                                                                                                                                                                                                                                             The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, preeclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the human gene regulation-associated genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to 224 nucleic acid sequences comprising at le 18 bases of a chemically pretreated gene associated with gene regula selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations.
                                                   6278
                                                                                                                                                                                                                                                                   Note:
of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
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30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID No 265; 26pp; English.
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                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                   420
                                                                                                                                                                                                                                  te: The sequence data for this patent did not form part the printed specification, but was obtained in electronic mat directly from WIPO at
cacatgcattttcaaacaaggaaaattaattctcaaaccaccatgacatgcaattctcaa
                                                                 ttttcccctctggaaattcatagctcacacttttttttaatggaagcaagagttggcaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-017470/02
                                                  TTTACCCACATCTCAACTTTTTTTTTTTTTTTTTTTTAAATTAACTACAAATTCCCAAA
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                                                                                                                               Similarity
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; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
                                                                                                                  Conservative
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Pred. No. 12;
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11-JUL-2000;
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vul
antiparkinsonian; antisickling; antianaemic; antiarthritic; cance
antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
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07-JUL-2000;
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24-FEB-2000;
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2000US-0225213.

2000US-0225214.

2000US-0225266.

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antiarthritic; cancer;
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(ABB1678-ABB18001) useful for preventing, treating or ameliorating commedical conditions e.g. by protein or gene therapy. The genes are consisted from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast candovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune contities; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and cepilepsy; and (f) infections.

Conte: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format Airnaria.
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Matches 69
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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1381 ggagactgctgtgagccaagatttcaccactgcactcagcctgggtgacagaccatgact 1440
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              717 ggagacgacgacgacaatcagacactcaccaactgcttttgtctggggacacaataaatgttt 776
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2000US-0249267
2000US-0249297
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diagnosing
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AAF22293/C
AAF22293 standard; DNA; 101786 BP.
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AC
AAF22293;
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AC
AAF22293;
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DT
20-MAR-2001 (first entry)
XX
BAC containing repeats from centrome
XX
Centromere; michrosome; vector; ds.
XX
Centromere; michrosome; vector; ds.
XX
Centromere; michrosome; vector; ds.
XX
Arabidopsis thaliana.
XX
W0200055325-A2.
YX
PN
21-SEP-2000; 2000WO-US07392.
XX
PP
17-MAR-2000; 2000WO-US07392.
XX
PP
18-MAR-1999; 99US-0125219.
PR
18-MAY-1999; 99US-0124409.
PR
13-SEP-1999; 99US-0134770.
PR
13-SEP-1999; 99US-0153584.
PR
17-SEP-1999; 99US-0154603.
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Preuss D, Copenhaver G, Keith K;
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17-SEP-1999; 99US-0154603.
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CUCH-) UNIV CHICAGO.
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PR
Recombinant DNA construct comprising producing stably inherited michrosom the construction of transgenic plant XX
CC The present invention relates to a j CC (Arabidopsis thaliana) centromere.
CC The producing stably inherited michrosom the construction of transgenic plant XX
SC (Arabidopsis thaliana) centromere.
CC The producing stably inherited michrosom the construction of transgenic plant SX
CC (Arabidopsis thaliana) centromere.
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        53503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells -
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370 tggaaattcatagctcacactttttttttaatggaagcaagagttggcaaacacatgcatt 429
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-08-999-646-1
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US-08-605-501-11
US-08-487-8268-13
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	Sequence 2: Sequence 1: Sequence 1: Sequence 1: Sequence 1: Sequence 1: Sequence 1: Sequence 7: Sequence 7: Sequence 7: Sequence 6: Sequence 6: Sequence 6: Sequence 6: Sequence 6: Sequence 7: Sequence 6: Sequence 6:
	22, Appl 10, Appl 10, Appl 10, Appl 10, Appl 10, Appl 10, Appl 17, Appl 17, Appl 17, Appl 17, Appl 17, Appl 16, Appl 16, Appl 27, Appl 16, Appl 16, Appl 16, Appl 16, Appl

Query Match

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DB 1;

Length 7218;

FILING DATE:

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APPLICANT: Alitalo, Kari
APPLICANT: JOUKOV, Vladimir
TITLE OF INVENTION: Vascular
TITLE OF INVENTION: Protein
                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F196/00427
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                  PRIOR APPLICATION NUMBER: 08/601,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                  PRIOR APPLICATION DATA:
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                                   APPLICATION NUMBER: FILING DATE: 12-JA
                                                                                                                                      APPLICATION NUMBER: 08/67 FILING DATE: 28-JUN-1996
                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 tttcttaaaagaacaggccatttaggccctgctttacaaaaggctcaaccagtccaaaac 132
                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   actggacagacgctcacgcaggagcccagcaccacaggcttgagcctgacagcggacgtg 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaattcatagctcacactttttttaatggaagcaagagttggcaaacacatgcattttc
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NUMBER:
                                   12-JAN-1996
                                                                                    14-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vascular Endothelial Growth Factor C (VEGF-C) Protein and Gene, Mutants Thereof, and Uses T 57
                                                   08/585,895
                                                                                                                                                    08/671,573
08/510,133
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South Wacker Drive
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RESULT 3
US-08-171-385-14/c
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                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5527884
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08171385 Patent No. 5527884
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Best Local Similarity 55.7%;
Matches 68; Conservative
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INFORMATION FOR SEQ ID NO:
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TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                 ATTORNEY/AGENT INFORMATION:
                                                                                                                   COMPUTER: IBM PS/2 Model 50Z or 55S;
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mary E. Russ
APPLICANT: Ulrike Utans
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LENGTH: 1741 base pairs
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ATTORNEY/AGENT INFORMATION:
                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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TELEFAX: 25-3856
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LOCATION:
 NAME:
                               APPLICATION NUMBER: FILING DATE:
                                                                          CLASSIFICATION:
                                                                                          FILING DATE:
                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                           CITY:
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                       STREET:
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Gass, David A.
Gass, NIMBER: 38,153
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RESULT 4
US-08-361-441B-14/c
; Sequence 14, Application US/08361441B
; Patent No. 6077948
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Best Local :
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REFERENCE/DOCKET NUMBER: 05.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
                                    APPLICATION NUMBER: 08/171,385
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 21-DEC-1994 PRIOR APPLICATION DATA:
                                                                                                                                                      OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Russell, Mary E. APPLICANT: Utans, Ulrike
            REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                           FITLE OF INVENTION:
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                                                                                                                                                US/08/361,441B
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                            05433/014001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-458-434A-6/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08458434A Patent No. 6083690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
            TELEFAX: 619-236-1048 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                        REFERENCE/DOCKET NUMBER: PO TELECOMMUNICATION INFORMATION: (619) 699-3604
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gosh-Choudhury Ph.D., Nandini
APPLICANT: Feng Ph.D., Jian Q.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
TITLE OF INVENTION: OSTEOGENIC AGENTS
NUMBER OF SEQUENCES: 13
                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weseman, James C.
REGISTRATION NUMBER: 30,507
                                                                                                                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: James C. Weseman,
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Harris Ph.D., Stephen APPLICANT: Mundy M.D., Gregory R.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     801 aa 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 TTAGAATTTATATATAAGAAAGAACATGTGGTGTTTCTTATTCTGAGTCTGGATTATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                 ZIP: 92101
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                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                          San Diego
                                                                                                                                                                                                                                                                                              CA
                                                                                                                                                                                                                                                                                                                          401 B. Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 base pairs
                                                                                                                                                                                                                                                                               USA
                           619-236-1048
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                                                                                                                                                           US/08/458,434A
             6:
                                                                                                                                                                                                                                                                                                                          Suite
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Pred. No. 0.
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                                                                                                                                                                                        Version #1.25
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LENGTH: 15144 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/08979608A Patent No. 635451
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11699 AACAAACTACAAATTTCCTTTTTTGGAAAATTTATATACAAACCCGATATTTCTTCTGAT 11640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11759 CAAGCACTTTGCTCAGCACCTTCCATGTAGACTTTGCATCTTAAATACACACAACTGAAA 11700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11639 TACATATAAATACAATTAACTAT 11617
                                                                                                              INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       526 atcaacatcccagttgtcgagtcgagaagaggatgacactgaaagtatgcgtattacgat 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  586 ttcatttacatacatgtacaaat 608
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nes 74; Conserv
                                                                                                                                                     REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5570
TELEFAX: 617/542-8906
                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/048,547
FILING DATE: 03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
  NAME/KEY:
                                    LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & Richardson P.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lees,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Law, Simon W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 Franklin Street
Coding Sequence
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51.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
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TELECOMMUNICALLAND TELECOMMUNICALLAND TELEFAX: (248) 539-5055 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 35060 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-814-095-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7 Patent No.
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Best Local 9
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                                                                                                                                               DESCRIPTION: NO
                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                            MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including
DESCRIPTION: promotor, ACHE gene and AF
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: TR
TITLE OF INVENTION: AN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                  ORGANISM: Homo s
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                  FEATURE:
                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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NAME/KEY: promoter LOCATION: 4089..22464 OTHER INFORMATION: /fivoTHER INFORMATION: /si
                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Montgomery, Ilene N. REGISTRATION NUMBER: 38,97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 63.0 nes 49; Conservative
                                                                                 CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Farmington Hills
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 GAGTGACCGTCCTGCAGGTGCCCAGCACCACCTTAACGGCGAGCGGGGACCTCAGAG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Application US/08814095 6025183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: KOHN & ASSOCIATES 30500 No. 6025183thwestern Highway, Suite
                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shani,
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                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSGENIC ANIMAL ASSAY SYSTEM FOR
 /function= "ACHE Promotor"
/standard_name= "ACHE Promotor"
                                                                                 7q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/814,095
                                                                                                                                                                                                                                                                                                                                                                                                 38,972
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Pred. No. 2.2;
0; Mismatches
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   "ACHE Promotor"
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FEATURE:
NAME/KEY: exon
LOCATION: 28008..28129
LOCATION: 28008..28129
IDENTIFICATION METHOD:
OTHER INFORMATION: /gen
OTHER INFORMATION: /num
                                                                                                                                                                                                 LOCATION: complement (34092...34358)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: exon
NAME/KEY: exon
LOCATION: complement (34528..34895)
OTHER INFORMATION: /function= "arser
OTHER INFORMATION: gene"
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 1
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LOCATION: 24090..25177
LOCATION: 24090..25177
LOCATION: MCTHOD: 
OTHER INFORMATION: /func
OTHER INFORMATION: /2411
OTHER INFORMATION: /genc
OTHER INFORMATION: /genc
OTHER INFORMATION: /numl
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NAME/KEY:
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                                    FEATURE:
                                                                                                                         FEATURE
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LOCATION: 22465..22
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAME/KEY: exon
LOCATION: 27255...28007
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 5
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LOCATION:
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OTHER INFORMATION: /ev
OTHER INFORMATION: /ge
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LOCATION:
NAME/KEY:
LOCATION:
                                                 NAME/KEY: exon
LOCATION: complement (33493...33591)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
                                                                                    NAME/KEY:
LOCATION:
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LOCATION: complement (33779...33963)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
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OTHER INFORMATION: /evidence= EX
OTHER INFORMATION: /gene= "AGHE"
OTHER INFORMATION: /number= 4
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27005..27274
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22465..22537
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27385..27387
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25524..26009
                  exon
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28129..28131
complement (33297..33408)
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/evidence= EXPERIMENTAL
/gene= "ACHE"
/number= 3
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/function= "(translation start:
24110)"
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/gene= "ACHE"
/number- 6
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/number= 1
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LOCATION: exon
LOCATION: complement (29664..29856)
COTHER INFORMATION: /gene= "ARS"
OTHER INFORMATION: /number= ''
US-08-814-095-7
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Best Local Similarity
Watches 72; Conserve
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
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LOCATION:
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LOCATION: complement (29945..30073)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 15
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
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LOCATION: complement (30816..31011)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
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LOCATION: complement (31131..31284)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 11
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
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LOCATION: complement (30187..30274)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
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LOCATION: complement (32569..32628)
OTHER INFORMATION: /gene= "AR"
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Pred. No. 23;
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Best Local Similarity
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APPLICANT:
APPLICANT:
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REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                            870 cgtcctcccgcacgcagcgtcgctccaccgtccgtcgttgctgctgtgctgtgc 929
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OPERATING SYSTEM:
SOFTWARE: PatentI
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TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: CH 0 FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                               ORGANISM:
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GTCG
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o. 6239264
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505
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Pohlmann, Kain.
Steiner, Sabine
Wohr, Christine
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Knechtle, Philipp
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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24-DEC-1997
                                                                                                                                                                                                                                                                           DNA (genomic)
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US-08-399-646-1
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Best Local S
Matches 63
Sequence 1, Application US/08607321 Patent No. 5716813
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                                                                                             1417 CCCGATCCGCAGGATCCGGAGACCTTCACCCGCTCCAAACTGGACTGGGCGGAAGC 1472
                                                                                                                                                           1357 GCCACGGCCGAGGGCAGCATCAGGGAGTTCGAGCGCATGGGGTGGGATCCCGCCGTCGTG 1416
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APPLICATION NUMBER: JP 5
FILING DATE: 07-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                820 gctaacggcatggccaggtaaacgcgctccccagccgttggttttgcgatctcgtcctcccg 879
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TELEPHONE: 202-737-3528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/O FILING DATE: 07-MAR-1995 CLASSIFICATION: 435
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSUSAKI, Keiji
HATTORI, Kazuko
SUGIMOTO, Toshiyuki
VENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
                                                                                                                                                                                                                        Conservative
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SYSTEM: PC-DOS/MS-DOS
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RESULT 11
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                                                   Sequence 1, Appli
Patent No. 583071
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Best Local :
                                  GENERAL INFORMATION:
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,321
FILING DATE: 26-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
FILING DATE: 07-MAR-1995
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MEDIUM TYPE: Floppy disk
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LENGTH: 1767 base pairs
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FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
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APPLICANT: SUGIMOTO, TOShiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: KUI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 59
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
   APPLICANT:
                                                                                                                                                                                   880 cacgcagcgtcgcctccaccgtccgtccgtcgctgccacctctgctgtgcgcgc 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                                                                                                                                                                                                                   820 gctaacggcatggccaggtaaacgcgctcccagccgttggtttgcgatctcgtcctcccg 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                           CCCGATCCGCAGGATCCGGAGACCTTCACCCGCTCCAAACTGGACTGGGCGGAAGC 1472
                                                                                                                                                                                                                                GCCACGGCCGAGGGCAGGATCAGGGAGTTCGAGCGCATGGGGTGGGGATCCCGCCGTCGTG 1416
                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                   Application US/08961240
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                                                                                                                                                                                                                                                                                                      Conservative
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KUBOTA, Michio
TSUSAKI, Keiji
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                        RESULT 12
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US-08-961-240-1
                                                                                                      Sequence 1, Applic Patent No. 5834287
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Best Local Similarity
Matches 63; Conserv
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
                                                                                   GENERAL INFORMATION:
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                                                 APPLICANT:
APPLICANT:
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FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
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MEDIUM TYPE: Floppy disk
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, TOShiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                     Application US/08605501
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419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1767 base pairs
                                                 KUBOTA, Michio
TSUSAKI, Keiji
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                                                                                                                                                                                                                                                                                                                                               Conservative
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DNA ENCODING ENZYME, RECOMBINANT DNA AND
ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/961,240
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Pred. No. 5.8;
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RESULT 13
US-08-399-646-11
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Best Local :
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APPLICANT: KUBOTA
APPLICANT: TSUSAK
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INFORMATION FOR SEQ ID NO:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
CORRESPONDENCE
                                                          APPLICANT: SUGIMOTO, TITLE OF INVENTION: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202-628-5197
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FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 59840
FILING DATE: 07-MAR-1994
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ANDRESSEE: BROWDY AND NEIWARK
ANDRESSEE: BROWDY AND NEIWARK
ANDRESSEE: BROWDY AND NEIWARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCACGGCCGAGGGCAGGATCAGGGAGTTCGAGCGCATGGGGTGGGATCCCGCCGTCGTG 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGATCCGCAGGATCCGGAGACCTTCACCCGCTCCAAACTGGACTGGGCGGAAGC 1472
                               OF SEQUENCES:
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                                                                                                                                                           TSUSAKI, Keiji
HATTORI, Kazuko
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                                                              D), Toshiyuki
DNA ENCODING ENZYME, RECOMBINANT DNA AND
ENZYME, TRANSFORMANT, AND THEIR PREPARAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/605,501
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Pred. No. 5
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                                                                 AND THEIR PREPARATIONS AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
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                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                        Sequence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                                                                                                                                                                               GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                            1584
                                                                                                 APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, Toshiy
TITLE OF INVENTION: DNA ENC
TITLE OF INVENTION: ENZYME,
                                                                                                                                                                                                                                                                                                  1644 CCCGATCCGCAGGATCCGGAGACCTTCACCCGCTCCAAACTGGACTGGGCGGAAGC 1699
                                                                                                                                  APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, Toshi
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LENGTH: 2161 base pairs
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                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-MAR-1994 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                        CITY: Washington
                                           STREET:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 5:
FILING DATE: 07-MAR-1994
COUNTRY:
                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 59840 FILING DATE: 07-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                            INFORMATION:
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             D.C.
                                                                                                                                                                                                                        Application US/08607321
                                         419 Seventh
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419 Seventh Street, N.W.,
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207..1994
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SYSTEM: PC-DOS/MS-DOS
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                                        BROWDY AND NEIMARK

3 Seventh Street, N.W.,
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                                                                                                     DNA ENCODING ENZYME, ENZYME, TRANSFORMANT,
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54.3%;
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Pred. No. 6.6;
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, AND THEIR PREPARATIONS AND USE
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SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

COMPUTER: IBM PC OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

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; LOCATION:
US-08-607-321-11
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US-08-961-240-11
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Best Local Similarity
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TELEX: 248633
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                                                                                                                        APPLICANT: TSUSAKI, Keiji
APPLICANT: HATTORI, Kazuko
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: DNA ENCODING ENZYME, F
TITLE OF INVENTION: ENZYME, TRANSFORMANT, SUGUENCES: 18
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 59834
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/607,321
FILING DATE: 26-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,646
FILING DATE: 07-MAR-1995
                                                                                                                                                                                                                        APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                    1584 GCCACGGCCGAGGGCAGGATCAGGGAGTTCGAGCGCATGGGGTTGGGATCCCGCCGTCGTG 1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                 880 cacqcaqcqtcqcctccaccqtccqtccqtcqctgccacctctqctqtqcqcqcqc
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TELEX: 248633
                                                                        STREET: 419 Seven
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TYPE: nucleic acid
STRANDEDNESS: single
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                                              COUNTRY:
                                                                                                            ADDRESSEE:
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                                   D.C.
USA
                                                                                            419 Seventh Street, N.W.,
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                                                                                                              BROWDY AND NEIMARK
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                                                                                             Suite 300
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..19:
US-08-961-240-11
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: KUTELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
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FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08
FILING DATE: 07-MAR-1995
APPLICATION NUMBER: UP 59
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                 1584 GCCACGGCCGAGGGATCAGGGAGTTCGAGCGCATGGGGTGGGATCCCGCCGTCGTG 1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2161 base pair
1644 CCCGATCCGCAGGATCCGGAGACCTTCACCCGCTCCAAACTGGACTGGGCGGAAGC 1699
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TELEFAX: Zv-
248633
                                           820 gctaacggcatggccaggtaaacgcgctcccagccgttggtttgcgatctcgtcctcccg 879
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TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BROWDY, Roger L. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: single
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54.3%;
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Search completed: September 12, 2002, 08:12:27 Job time: 14804 sec

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Minimum
Maximum
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Perfect score:
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                    Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1101)
                                                                          Contact: Genoscope
                                                                                         Unpublished (2001)
                                                                                                    Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
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Matches 62
                                                                                                                                                                                                                                                                          AUTHORS
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melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BOED Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
                                                                                                                                 Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                                                                         Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 844)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNSUU52P 844 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR11016 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;

    Web : www.genoscope.cns.fr)

                                                                                                                                                                                                                                                                                                 Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                   fruit fly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
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/db_xref="taxon:9606"
/db_xref="CLOBA002ZA07"
/clone="CLOBA002ZA07"
/clone_llb="LTT_NFL006_PL2"
/tissue_type="placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:4932342
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Pred. No.
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                                                                                                                                                                                                                              segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSSYCTYCYSSCCBYCCBSGCBTBSYB
                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortiu
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution in Clone distribution: NCI-CGAP clone distribution in found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 931)
                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                   BF142642.1 GI:10981682
                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601789378F1 NCI_CGAP_Lu30
                                                                 High quality sequence stop: 663.
                                                                                http://image.llnl.gov
Plate: LLAM9273 row: k column:
                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                    house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR11P16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="end : TET3"
112 c 92 g
/strain="CZECH
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                  /organism="Mus
                                                 Location/Qualifiers
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musculus"
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                                                                                                                                                                                                                                                                                                                                              USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, UTel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 427)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG895352 427 bp mRNA
358754 MARC 1PIG Sus scrofa cDNA 5', mRNA
BG895352
BG895352.1 GI:14305593
                                                                                                                                                                                                                                                                           Single pass sequencing. Bases c
v0.980904.e. Vector identified
                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
Email: smith@email.marc.usda.gov
cingle pass sequencing. Bases called and alt_trimmed
                                                                                                                                                                                                                                                                                                                                                                                                               Design and use of two pooled tissue EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                          Seq
                                                                                                                                                                                                                                                                                                                               Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa
                                                                                                                                                                                            Plate: 122 row: L column:
                                                                                                                                                                                                            BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                           FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                               PCR PRimers
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/note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI; Library made from pooled tissue from day 11, 13, 15, 20 and 30 embryos."
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/lab_host="DH10B"
                                                                                    /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:4020235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Lu30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
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Pred. No. 25;
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                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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IMAGE:337805
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                                                                                                                                                                                                                                   quality sequence stop: 166
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                                                  double-stranded cDNA was size selected, ligated to Eco adapters (Pharmacia), digested with Not I and cloned in
(Pharmacia). Library went through one round
             the Not I and Eco RI sites of a modified pT7T3 vector
                                                                                                                                                          /clone="IMAGE: 337805"
                                                                                                                                                                            /db_xref="taxon:
                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                       Location/Qualifiers
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Soares mouse p3NMF19.5
05 5', mRNA sequence.
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Pred. No. 66;
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HVSMEm0012M10f Hordeum vulgare green seediling Lucy Cone vulgare cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total hq bases = 137
Total hq bases = 137
Seq primer: AATTAACCCTCACTAAAGGG
Seq primer: ASTUALCCTCACTAAAGGG
Seq primer: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 Jordan Hall, Clemson, Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Ran,J., Oates,R. and Main,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhOI; Morex (mla) plants were greenhouse grown in the R Wise lab at lowa State University, Ames, IA, 7 day old green seedlings were infected with isolate 5874 of Blumeria graminis f. sp. hordei, and leaves were harvested 24, 48 and 72 hr post-inoculation and snap frozen is the state of the state of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

178 c 424 g 258 t 20 others
                                                                                                                                                                                                                                        /tissue_type="green seedling leaf"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                              HVcDNA0014 (Blumeria infected)
                                                                                                                                                                                                                                                                                                                                                          /clone="HVSMEm0012M10f"
/clone_lib="Hordeum vulgare green seedling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Hordeum vulgare"
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Pred. No. 68;
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RESULT 8
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BOHUA13TR BOHU Brassica
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                                                                                                                                                                                                                                                                                         Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophy
Spermatophyta; Magnoliophyta; eudicotyledons; cor
Rosidae; eurosids II; Brassicales; Brassicaceae;
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                                                                                                                                                                                                                                                      Contact:
                                                                                                                                                                                                                                                                        Other_GSSs: BOHUA13TF
                                                                                  Class: sheared ends.
                                                                                                                        Email: cdtown@tigr.org
DNA is from a doubled haploid
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                                                                                                                                                                     301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
a 161 c 512 g 87 t
                                                                                                                                                                                                                                                      Chris Town
/organism="Brassica oleracea"
/strain="TO1000DH3"
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                                           Location/Qualifiers
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Pred. No. 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF980551 1098 bp mRNA linear EST 23-JAN-2 602304314F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4395795 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence
BF980551
                                                                                                                     Tissue Procurement: ATCC
                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                           National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                            NIH-MGC http:
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1098)
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a 46 c 55 g 205 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3712"
/clone="BOHUA13"
                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4395795"
/tissue_type="duodenal adenocarcinoma,
/lab_host="DH10B (phage-resistant)"
                           /clone_lib="NIH_MGC_88"
                                                                                                        Location/Qualifiers
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Determination of this BAC-end sequence was carried out as part of collaboration with the Beckeley Drosophila Genome Project (BDGP)

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's Laboratory in the Department please see http://www.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org.fruitfly.org
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Tel: 301 838 0200

Fax: 301 838 0208

Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end_search page: http://www.tlgr.org/tdb/humgen/bac_end_search/bac_end_search.html.

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                                         Similarity
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                                                                                                                                                                                                     /cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; EcoRI; Site_2: EcoRI; EcoRI; Site_2: EcoRI; EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:7572720"
/db_xref="taxon:9606"
/clone="RPCI-11-190G1"
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Score 37.8; DB Pred. No. 1.1e+ 0; Mismatches
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                                                                                               L1, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope Genoscope - Centre National de Sequencage Bp 191 91006 EVRY cedex - France Email: segref
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                                                                                                                                                                                                                                                                                             http://fulllength.invitrogen.com"
a 393 c 245 g 106 t 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="CSODIO18YJ18"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
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AG043219 1477 bp DN/
Pan troglodytes DNA, clone: PTB-021H1;
AG043219 AG043219.1 GI:16571944
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes DNA, clone: PTB-068E17.F, genomic su AG0754011 GI:16627203 GSS; GSS (genome survey sequence). Pan troglodytes male lymphoblast DNA, clone_lib:PTB BAC Library clone:PTB-068E17.F.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
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/sex="male"
/cell="male" | /cell | /cell
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/db_xref="taxon:9598"
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Pred. No. 1.1e+02;
0; Mismatches 53;
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PTB-021H12.F,
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      clone_lib:PTB Chimpanzee Male
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Best Local Similarity 55.1%;
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   Mouse
                   and Fraser,C.M. Mcgann,S.,
                                                                         Mus musculus
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 471)
                                                                                                                                                                   GSS
                                                                                                                                                                                                                                       AZ113002 471 bp DNA linear GSS 12-MAY-2000 RPCI-23-13D17.TJ RPCI-23 Mus musculus genomic clone RPCI-23-13D17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Tel:81-45-503-9111, Fax:81-45-503-9170 BAC library PTB This BAC end Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                       Zhao, S., Nierman, W., Feldblyum, T.,
                                                                                                                                                                                     AZ113002.1 GI:7772220
                                                                                                                                                                                                                     DNA sequence.
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                                                                                                                                                  house mouse.
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
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/db_xref="taxon:9598"
/clone="PTB-021H12.F"
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Pred. No. 1.2e+02;
0; Mismatches 57;
from Library RPCI-23
                                lyum,T., Malek,J., Sha
Tsegaye,G., Geer,K.,
                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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41 others
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                                                                                                                     AGGAGTAAGGTTAAGAATCCAACCATTCTGGGTTG 373
                                                                                                                                                              acaaggaaaattaattctcaaaccaccatgacatg 469
                                                                                                                                                                                                           ATTCATCGGTCACGCCATTTTTTAATGTAACCAATAGTTCTAGATCCCATGGCTTGGTTG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 13 row: D column: 17 Seq primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research 9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other_GSSs: RPCI-23-13D17.TV
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                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-*Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " a 129 c 97 g 113 t
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/clone="RPCI-23-13D17"
/clone_lib="RPCI-23"
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/strain="C57BL/6J"
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Pred. No. 1.3e+02;
0; Mismatches 36;
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KEYWORDS
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ORGANISM
Aegilops tauschii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
REFERENCE
AUTHORS
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GOODMAN FIELDER LTD (AU); LI ZHONGYI (AU); MORELL MATTHEW (AU);
RAHMAN SADEQUR (AU); GROUPE LIMAGRAIN PACIFIC PTY L (AU)
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1 (bases 1 to 11475)
Rahman,S., Regina,A., Li,Z., Mukai,Y., Yamamoto,M.,
Rahman,S., Regina,A., Li,Z., Mukai,Y., Yamamoto,M.,
Kosar-Hashemi,B., Abrahams,S. and Morell,M.K.
Comparison of Starch-Branching Enzyme Genes Reveals Evolutionary
Relationships Among Isoforms. Characterization of a Gene for
Relationships Among Isoforms. The Wheat D Genome Donor Aegilops
Starch-Branching Enzyme IIa from the Wheat D Genome Donor Aegilops
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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NADTWTRDDYGVWEIFLPNNADGSSAIPHGSRYKIRMDTPSGVKDSISAWIKESVQAP
GEIPFNGIYYDPPEEEKYVFQHPQRKRPESLRIYESHIGMSSPEPKINSYANFRDEVL
PRIKBLGYNAYQIMAIQEHSYYASFGYHVTNFFAPSSRFGTPEDLKSLIDRAHELGIL
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GDIVHTLTNRRWLEKCVTYAESHDQALVGDKTIAFWLMDKDMYDFMALDRPSTLRIDR
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LVFVFNFHWSNSFFDYRVGCSKPGKYKVALDSDDALFGGFSRLDHDVDYFTTEHPHDN
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                                               attttcccatcctaaatggcagggccctatcgccgaatatttttccattctatatattg
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TITLE
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AJ000497
AJ000497.1 G
Sbe2.1 gene;
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Uppsala Genetic Center,
7055, s-75007 Uppsala, s
2 (bases 1 to 7020)
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                                                                    /translation="MVYTISGVRFPHLPSIKKNSSLHSFNEDLRRSNAVSFSLRKDS
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PSGIKDSITAMIKYSVQPPGEBIPYNGVYVDPDEEDKYAFKHPRFKKFTSLRIYESHVG
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4234. .4355,4501. .4620,4716. .4845,4965. .5075,5193.
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4234. 4355,4501. 4620,4716. 4485,4965. 5075,5193.
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                                                                                TGGCTTCTCTTTAA 4638
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                                                                                                     ttagtccaatttaa 746
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AC006919 101365 bp DNA linear PLN 05-APR-2000 Arabidopsis thaliana chromosome II section 199 of 255 of the complete sequence. Sequence from clones F2H17, F1O11, F13K3.
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6436. 6519
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Pred. No. 8.5e-22;
0; Mismatches 138;
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exon

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intron

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exon

intron

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
PUBMED
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                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                   F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by two proteins are organized that the sequence of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09 MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA on Dec 17, 1999 this sequence version replaced gi:4581138. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 101365)
Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D., Fujii, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Feldblyum, T.Y., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M., Koo, H., Moffat, K.S., Cronin, L.A., Shen, M., Vanaken, S.E., Umayam, L., Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H., Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes were identified by a combination of three methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter,J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC006919 AE002093
AC006919.5 GI:65
                                                                                                                                                                                                                         Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted by tRNAscan-SE (Sean Eddy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin, X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402 (6763), 761-768 (1999)
                                                                                                                                                                                                                                                                                                   This work was supported by the National Science Foundation
Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dentified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 101365)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from the top to bottom of the chromosome.
/db_xref="taxon:3702"
/chromosome="II"
                                                                                         /organism="Arabidopsis thaliana"
                                                                     /cultivar="Columbia
                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:6598632
                                                                                                                                                                                                                                                                                               Energy
                                                                                                                                                                                                                 at@tigr.org
                                                                                                                                                                                                                                                                                           Department of
                                                                                                                                                                                                                                                                                               Agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for sequencing clone
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misc_feature
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                                                                                                                                        LENVTILLES LIGHTLES KKRKI EILKDISGI IKPSKMTLLIGPPSSGTTLLGA
LAGKLDDTLGMSGR TY CGHERREFVPQKTCAY ISQHDLHFGEMTVRESIDESGRCIG
VGTRYQLLTELSGREREAG IKPDPEIDAFMKSIAI ISQGETSLVTDYVLKLLGLDICAD
TLVGDWARRGI SGGORKRLTTGEMLVGBATALFMDE ISTGLDSSTTFOLCKFMROLVH
IADVTMVISLLQPAPET FELFDDIILLSEGQIVYQGSRDNVLEFFEYMGFKCPERKGI
ADFLGEVTSKKDQEQYMNRREHPYSYVSYHDFSSGFNSTHAGQQLASEFRVYDKAKT
HPAALVTQKYGISNKDLFKAGEDREMLLMKRNISFVYDFKTRVQITINSLIAMVYVFRTE
MHVGTVQKGKYGALFFSLINLMFNGMAELAFTVMRLPVFFKQRDFLFYPDWAFALP
GFLLKIPLSLLESVTWIALTYYTIGFAPSAARFFRQLLAFCVNQMALSLERFLGALG
RTEVIANSGGTLALLVVFVLGGFIISKDDIPSWLTMYCYTSPMMYGQTALVINEFLDE
RWGSPNNDTRINAKTVGEULLKSRGFFTEPYWFWICIGALLGFTVLENFCYIIALMYL
NPLGNSKATTVVEEGKDKHKGSHSGTGVELTSTSSHGRKGMYLPPQPLSLAFNNNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="F2H17.2; predicted by genscan"
join(304. .486,563. .613,1357. .1445,1521. .1626,1770. .1806
1886. .2037,2371. .2794,3184. .3312,3391. .3536,4096. .4314,
4639. .4719,4850. .4894,4936. .5055)
/gene="At2936370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="At2g36380"
//gene="At2g36380"
//note="F1011.1; related to multi drug resistance proteins and P-glycoproteins"
join(10119. 10507.10609. 10729,10984. 11157,11243. 111
11613. 11703,11793. 112994.12303. 113133,
11616. 113381,13466. 112543,13266. 113735,13825. 14157,
14244. 14534,14613. 14996,14771. 14904,14986. 115213,
15298. 115469,15550. 115804,15894. 16163)
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/note="Sequence from Clone F2H17"
/note="Sequence from Clone F2H17"
join(<304. .486,563. .613,1357. .1445,1521. .1626,1770. .180
1886. .2037,2371. .2794,3184. .3312,3391. .3536,4096. .4314,
4639. .4719,4850. .4894,4936. .>5055)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="(TA)n"

join(<10119. .10507,10609. .10729,10984. .11157,11243. ...

join(<10119. .10507,10609. .10729,10984. .11157,11243. ...

join(<10119. .10507,10609. .10729,10984. .11157,11243. ...

11613. .11703,11793. .12693,12781. .12941,13030. .13133,

13216. .13381,13466. .1543,31366. .13735,13825. .14157,

14244. .14534,14613. .14696,14771. .14904,14986. .15213,

15298. .15469,15550. .15804,15894. .16203)
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complement(9283. .9377)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mlgrdedlvrtmsgrgslgstshrslagaasksfrdvfapptddvfgrsdrreeddvelrwaalerlptydrlrkgmlpQtmvngkigledvdvtnlapkek
khlmemilkfyeednekflrrlrertdrvgievpkievryenlsyegdvrsasralpt
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ELSLECGSITENGVASLYGCIALEDLFLRHNGSGIQKSFLLDATLKRFFCLIHLNNEQ
Y VBGS IN 15GYPKNOATFARYSGYCEONDIHSPHYTVE ESLYGAWLRISADIDTKTR
Y VBGS IN 15GYPKNOATFARYSGYCEONDIHSPHYTVE VELVANPS II FEMDEDTSG
EMFVEEVMELVELKPLRNS I YGLPGVDGLSTEORKRLTI AVELVANPS II FEMDEDTSG
LDARRAAN I VARTVRTYDDTGRTVVCTI HQPS I DI FESFDELLLMKRGGQVI Y AGTILAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative ABC transporter"
/protein_id="AAD24623.1"
/db_xref="GI:4581139"
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/db_xref="GI:6598633"
                                                                                                            YVDMPAEMKAQGVEGDRLQLLRDVGGAFRPGVLTALVGVSGAGKTTLMDVLAGRKTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="At2g36380"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .101164
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                                                                                                                   433
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    553
                                                                                                                                                                           373
                                                           493
                                                                                                                                                                                                                                                                           Local Similarity
acaactacacttagtattctgaaaaagatcattttattgttgttggcttgttccaggtac 612
                                                                                                                tttgggtattcacacaatccatttttttctgtatacactcttcacccatttggagctatt 492
                                                                                                                                               AAGCTAGGCTATAATGCTGCAGATAATGGCCATTCAAGAGCATGCCTACTATGCCAGC
                                                                                                                                                            AATGAATACCTGTTAAAAGCCATTTGTTGATTCTTCAGAGTC
                                                        acatcctaatgcttcatgcacataaaatatttggatataatcctttattagatatatagt 552
                                                                                                                                                                                                                                                               270;
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18346. 18388 18859. 18918. 19163. 17898,18091. 1
18346. 18388 18859. 18918,19105. 19185,19275. 19391,
19607. 19690, 20048. 20169, 20315. 20434,20530. 20659,
20778. 20888 21006. 21134,21217. 21320,21415. 21559,
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/produr--".
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20778. .2
21691. .2
                                                                                                                                                                                                                                                                                                                                  complement(22710.
/gene="At2g36400"
/note="F1011.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVADKWIELLKKRDEDWQVGDITFTLINRRWGEKCVVYAESHDQALVGDKTIAFWLMD KDMYDFMAVDRQATPRVDRGTALHKMIRLITWGLGGEGYLNFW.OREFGHPEWIDFPRT DQHLPDGRVIAGNNGSYDKCRRRFDLGDAEXLLKHGLQFEDRAMQNLEETYGFMTSHDQHLPDGRVIAGNULETYGFMTSHTHWTNSYSDYRIGCSVPGKYKIVLDSDNSLFGGFNRLDDSAEFFTSDGRHDDRPCSFMVYAPCRTAVVYAAVDDDDDDERSSLVPIGLLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVLFCLLEWQTGTKIEKEQDLINNEFGAMYAAVLELGATNAATVQPAVALERTTVEYREK
AAGMYSAIPYAISQVAVEIMYNTIQTGVYTLILIXSMIGYDWTYOPEWFYYYMASPVAW
YETLYGMMLYALTPNYQIAGICLSFELSEWILFSGELLERPQIEIWWRWYYMASPVAW
TLYGIITSQVGDRDSIVHITGVGDMSLKTLLKNGEGEDYDELPVVAVVHIAWILIFLF
                                                                                                                                                                                                                                                                                                                     complement(join(22836. .23271,24081. .24435,24650.
                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(19524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="starch branching enzyme
/protein_id="AAD24644.1"
/db_xref="GI:4581160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(16662.
                                                                                                                                                                                                                                                                                                                                                                            /gene="At2g36400"
                                                                                                                                                                                                                                                                                                                                                                                                        complement(
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18346. 18388,18859. 18918,19105. .19185,19275. .19391,
19607. .19690,20048. .20169,20315. .20434,20530. .20659,
20778. .20888,21006. .21134,21217. .21320,21415. .21559,
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                                                                                                                                                                                                                                                                                                                                                                                                       _family="(TA)n"
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                                                                                      -CTTCCTTTCTCAGATATAACATGTCTACCTACCTATCATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/
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Bevan,M., Pohl,T., Weizenegger,T.,
Rudd,S., Lemcke,K. and Mayer,K.F.X.
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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VEFIVEDIHCNESYSDLVRLHNESLKKAVAKLNKEDKFRTKGDRFVIVDLHKAFMTIL
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/variety="Columbia"
                                                                                                                                                                                        translation="MKPTALSWKLPYGITFPGKPSGRYSDGLTATDFLGSEVFDSPVD/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aattaaaaggcttggatacaatgcagtgcagataatggcaatccaggagcattcatacta 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttgttcttatggatattgttcataggtaatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGCCATTTCTATTATGAATGCAGGTACCATGTCACAAACTTTTTTTGCCCCAAGCAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atatagtacaactacacttagtattctgaaaaagatcattttatt------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agctattacatcctaatgcttcatgcacataaaatatttggatataatcctttattagat 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-AUG-1996) University of Hamburg, Institute of Gener Botany, Centre of Applied Molecular Biology, AMP II, Ohnhorststr. 18, Hamburg 22609, Germany
                                                                                                                                                                                                                                                                                                                                     Kroeger, C., Loerz, H. and Luetticke, S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poiddeae; Triticeae; Triticum.

1 (bases 1 to 2853)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAU66376 2853 bp m
Triticum aestivum 1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U66376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6-alpha-D-(1,4-alpha-D-glucanotransferase mRNA, complete cds
/translation="MTGGTAEKLQSSEPTQGIVETITDGVTKGVKELVVGEKPRVVPK
PGDGQKIYEIDPTLKDFRSHLDYRYREYKRIRAAIDQHEGGLEAFSRGYEKLGFTRSA
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6-alpha-D-(1,4-alpha-D-glucanotransferase"
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                                                                                                                   /codon_start=1
                                                                                                                                 /note="branching enzyme"
                                                                                                                                                  /EC_number="2.4.1.18"
                                                                                                                                                                                   /db_xref="taxon:4565"
/tissue_type="kernels
                                                                                                                                                                                                                                     /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:1620661
                                                                                                                                                                                                                    'cultivar="T.A. Florida"
                                                                                                                                                                                                                                                                    ocation/Qualifiers
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Pred. No. 9.7e-20;
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Matches 136
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                                                                                                                                                                                                                                                                                                                                          Submitted
Stockholm
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AF064560
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sun,C., Sathish,P., Ahlandsberg,S. and The two genes encoding starch-branching differentially expressed in barley plant Physiol. 118 (1), 37-49 (1998)
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Hordeum vulgare cultivar Bomi starch branching
                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                              Sun,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
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Hordeum vulgare
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ilarity 91.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nuclear gene
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IYESHIGMSSPEPKINSYANFROEVLPRIKKLGYNAVQIMAIGERSYYASEGYHYTNF
FAPSSRFGTPEDLKSLIDRAHELGLLVLMDIVHSHSSNNTLDGLNGFDGTDTHYFHGG
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FTRSAKGITYREWAPGAHSAALVGDFNNWNPNADTMTRDDYGVWEIFLPNNADGSPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFMTSEHQYVSRKHEEDKVIIFERGDLVFVFNFHWSNSFFDYRVGCSKPGKYKVALDS
DDALFGGFSRLDHDVDYFTTEHPHDNRPRSFSVYTPSRTAVVYALTE"
3 585 c 746 g 746 t
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IAFWLMDKDMYDFMALDRPSTPRIDRGIALHKMIRLVTMGLGGESYLNFMGNEFFGHPE
WIDFPRGPQTLPTGKVLPGNNNNYDKCRRRFDLGDAEFLRYRCMQEFDQAMQHLEEKY
                                                                                                                                /gene="sbeIIa"
/EC_number="2.4.1.18"
                                                                                                                                                                                                                                                                                                                                          (11-MAY-1998) Stockholm University, Biochemistry, S-10691, Sweden
                                                                                                                                                                                      /gene="sbeIIa"
                                                                                                                                                                                                                           /db_xref="taxon:4513"
/chromosome="2"
                                                                                                                                                                                                                                                                                     /organism="Hordeum
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                    /cultivar="Bomi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticeae; Hordeum.
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Pred. No. 7.7e-19;
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Kosar-Hashemi,B., Abrahams,S. and Morell,M.K.
Comparison of Starch-Branching Enzyme Genes Reveals Evolutionary
Relationships Among Isoforms. Characterization of a Gene for
                                                                                                                                                                                                                                                                                                            Submitted (18-JAN-2001) Plant Industry, CSIRO, Canberra, ACT 2601, Australia
                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 2726)
Rahman, S., Regina, A., Li, Z., Abrahams, S. and Morell, M.K.
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21140316
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1 (bases 1 to 2726)
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KFHGGFRGHHWMDSRLENYĞSWEVLRFLLSNARWALEEYKFDGFRFDGVTSMYTHH
GLQMTFTGNVGEYFGFATDVDAVVYLMLVNDLHGLYEDAVSIGEDVSGMPTFCI IVP
DGGVGFDYRLHMAVADKWIELLKQSDESWKMGDIVHTLINRRWLEKCVTYAESHDQAL
VGDKTIAFWLMKDMYDFMALDRPSTPRIDRGIALHKMIRLYRMGLGGEĞYLMFMGNE
FGHPEWIDFPRGPQTLPTGKVLPGNNNSYDKCRRRFDLDADFLRYGMQEFDQAMQH
LEEKYĞFMTSEHQYVSRKHEEDKVI IFERGDLYFVFNFHWSNSKKDYRYĞCSKPGKYK
VALDSDDALFGGFSRLDHDVDXFTTEHPHDNRPRSFSVYTPSRTAVVYALTE"
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/db_xref="taxon:4565"
124. .2430
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                                                                                       /product="starch branching enzyme IIa variant"
/protein_id="AAK26822.1"
/db_xref="GI:13447952"
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PESLRIYESHIGMSSPEPKINSYANFRDEVLPRIKRLGYNAVQIMAIQEHSYYASFGY
                                                                                                                                                       /codon_start=1
                                                                                                                                                                                /note="SBEIIa variant"
                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  attgttcataggtaattagtccaatttaattttagctgtttttactgttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTGTTCATAGTCATTCATCAAATAATACCCTTGACGGCTTGAATGGTT
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McCue, K.F., Hurkman, W.J., Tanaka, C.K. and Anderson, O.D.

Starch Branching Enzymes Sbel and Sbe2 from Wheat (Triticum aestivum cv. Cheyenne): Molecular Characterization, Developmental Expression, and Homolog Assignment by Diffferential PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF286319
Triticum
                                                                                                                                                                                                                                                                                                                                                                             Submitted (11-JUL-2000) United Agricultural Research Service,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyi Spermatophyta; Magnoliophyta; Liliopsida; Poales; Pooldeae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF286319.1
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                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 2970)
McCue, K.F. and Anderson, O.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bread wheat.
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AHELGLLVLMDIVHSHSSNNTLDGLNGFDGTDTHYFHGGPRGHHMMDSRLFNYGSWE
VLRFLLSNARMHLEEYKFDGFRFDGVTSMMYTHGLQMFTFTGNYGEYFGFATDVDAVV
YLMUDLIHGLHPDAVSIGEDVSGMPTFCIPVDGGVGFDYRLHMAVADKWIELLKQ
SDESWKMGDIVHTLTNRRWLEKCVTYAESHDQALVGDKTIAFWLMDKDMYDFMALDRP
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NNNSYDKCRRRDDLGDADFLRYIGMQEFDQAMQHLEEK'GFMTSEHQYVSSKHEEDKV
IIFERGDLVYVENEHWSMSFEDYKYGGGRPGKYKVALDSDDALFGGFSRLDHDVDYFT
TEHPHDNRPRSFSVYTPSRTAVVYALTE"
                                                                               alpha-1,4-glucan-6-glucosyltransferase"
                                                                                                   /gene="Sbe2"
/EC_number="2.4.1.81"
/note="glucosyltransferase;
/product="starch branching enzyme
/protein_id="AAG27623.1"
/db_xref="GI:11037534"
                                                                                                                                                                     /gene="Sbe2"
149. .2620
                                                                                                                                                                                                                                                    /organism="Triticum aestivum"
/cultivar="Cheyene"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFSVQAPGEIPFNGIYYDPPEEEKYVFQHPQPKRPESLRIYESHIGMSSPEPKINSYA
                                                                                                                                                                                                                                                                                                                    Cocation/Qualifiers
                                                             /codon_start=1
                                                                                                                                                                                                               tissue_type="endosperm"
|. .2970
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Pred. No. 6.1e-18;
0; Mismatches 28
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                                                                                                                                                                                                                                                                                                                                                                                States Department of Agriculture, 800 Buchanan Street, Albany, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA linear PLN : enzyme 2 (Sbe2) mRNA,
                                                                                                       alpha-1,4-glucan;
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                                                                                                                                                                                                                                                                     Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology Institute, National Research Council of Canada, 110 Gymnasium Place, Saskatoon, Saskatchewan S7N 0W9, CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                          Isolation, characterization and expression analysis of a starch branching enzyme II cDNA from wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bread wheat.
Triticum aestivum
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enzyme II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T.aestivum mRNA for starch branching
                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nair, R.B., Baga, M., Scoles, G.J., Kartha, K.K. and Chibbar, R.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y11282.1 GI:1885343
                                                                                                                                                                                                                                                                                                                                                                                                      Plant Sci. In press
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YRYSEYRRIRAAIDQHEGGLEAFSRGYEKLGFTRSAEGITYREMAPGAISAALVGDFN
NWNPHADTMTRDDVGYWEIFLANNDCSPALFHGSRVKLRMOTPSGVKDSISANIKFN
VQAPGEIPFNGIYVDPPEEEKVVFQHPQPKRPESLRIYESHIGMSSPEPKINSYANFR
DEVLPRIKTLGYNDVOLMAIOEHSYYASFGYHTVNFFAPSSRFOTPEDLKSLIDRAHE
LGLLVLMDIVHSHSSNNTLDGLMFFDGTTHYFHGDFRCHHWWDDSRLFNGSWEVLF
ELLSLARRWWLEEYKFDGFRFDGVTSMYTHHLLOMTFTGNYGBYFGFATDVDAVVYLM
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ERGDLVFVFNFHWSNSFFDYRVGCSRPGKYKVALDSDDALFGGFSRLDHDVDYFTTEH
PHDNRPRSFSVYTPSRTAVVYALTE"
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SWKMGDIVHTLTNRRWLEKCVTYAESHDQALVGDKTIAFWLMDKDMYDFMALDRPSTP
RIDRGIALHKWIRLVYMGLGGEGYLNFMGNEFGHPEWIDFPRGPQTLPTGKVLFGNNN
                                                           /gene="sbe2"
151. .312
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KDSSRAVLSRAASPGKVLVPDGESDDLASPAQPEELQIPEDIEEQTAEVNMTGGTAEK
/gene="sbe2"
                   /gene="sbe2"
151. .2622
                                                                                                        /dev_stage="kernels 12
151. .2948
                                                                                                                                                                    /db_xref="taxon:4565"
                                                                                                                                                                                        /organism="Triticum aestivum"
/cultivar="Fielder"
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                             /clone="pRN33"
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                                                                                                                         days post anthesis"
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e II.
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RESULT TASBA2

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KEYWORDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 598 gcttgttccaggtaccatgttactaatttttttgcaccaagtagccgttttggaactcca 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    718
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                                                                                                                                                                                                                        Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                Zea mays
AF072725
                                                                                     Kim,K.-N., Fisher,D.K., Gao,M. and Guiltinan,M.J. Molecular cloning and characterization of the amy encoding starch branching enzyme IIb in maize
                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 Submitted (16-JUN-1998) The
                                  Kim, K.-N., Fisher, D.K.,
                                                         Unpublished 2 (bases 1
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                   Direct Submission
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                                                      (bases 1 to
                                                                                                                                               (bases 1 to 23449)
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2948
                                                                                                                                                                                                                                                                                                                   starch branching enzyme
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2930. .2935
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/product="1,4-alpha-glucan
2879. .2884
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IGELVUMDIVHSHSSNNTLDGLNGFDGTDTHFFAPGSRFGHHWMDSRLFNYGSWEVLK
FLLSNARWHLEEYKFDGFRFDGVTSMNYTHHGLQMFTGHVGEYFGFATDUDAVVLK
LVNDLIHGLHPDAVSIGEDVSGMFTFCIPVPDGGVGLDYRLHMAVADKWIELLKQSDE
SWKMGDIVHTLTNRWLEKCVTYAESHDALVGDKT AFWLLNUMYDFMALDRPSTP
RIDRGIALHKHIRLVTWGLGGESYLAFMGNEFGHPEWIDFPRGPGTLDFSTLVLGKNUN
SYDKCRRRFDLGDADFLRYHGMQEFDQAMQHLEEKYGFMTSEHQYVSRKHEEDKVIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SpTrembl:p93691"
/translation="MATFAVSCATILGVARPAGAGGGLLPRSGSERRGGVDLPSLLLRK
/translation="MATFAVSCATILGVARPAGAGGGLLPRSGSERRGGVDLPSLLLRK
KDSSRAVLSRAASPGKVLVPDGESDDLASPAQPEELQIPEDIEEQTABVNMTGGTAEK
KDSSEPTQGIVETITDGVTKGVKELVVGEKPRVPKPGDGQKIYEIDPTLKDFRSHLD
YRYSEYRRIRAAIDQHEGGLEAFSRGYEKLGFTRSAEGITYREMPGAHSAALVGDFN
YRYSEYRRIRAAIDQHEGGLEAFSRGYEKLGFTRSAEGITYREMPGAHSAALVGDFN
NWNPHADTMTFADDYGVWEIFIFPNHOGSPAIPHGSRVKIRMJTPSGVUKDISANIKFS
VQAPGEIPFNGIYYDPPEEEKYVFQHPQPKRPESLRIYESHIGMSSPEPKINSYANFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="1,4-alpha-glucan
/protein_id="CAA72154.1"
/db_xref="GI:1885344"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERGDLVFVFNFHWSNSFFDYRVGCSRPGKYKVALDSDDALFGGFSRLDHDVDYFTTEH
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83.4%;
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                                                                                                                                                                                                                                                                                                                                      23449 bp
                                    Gao, M.
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Biotechnology Institute,
                                    and Guiltinan, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      773
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                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                            amylose-extender gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enzyme
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 Pennsylvania
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                          429
                                                                                                                     369
                                                                                                                                                                                                              309
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aagctttgggtattcacacaatccattttttttctgtat 4
                                                                                             taaaaggcttggatacaatgcagtgcagataatggcaatccaggagcattcatactatgc 428
                                                                                                                                                                                        tgcacaggaaccgaagataaattcatatgctaattttagggatgaggtgttgccaagaat 368
                                                                     AAAAAAACTTGGATACAATGCAGTGCAAATAATGGCAATCCAAGAGCACTCATATTATGG
                                                                                                                                                                TGATTAGGAACCGAAGATAAACACATATGTAAACTTTAGGGATGAAGTCCTCCCAAGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                    6409
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="ae"
19879
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a 4892 c
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/gene="ae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="ae"
19843. .198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADGTSPIPHGSRVKVRMDTPSGIKDSIPAWIKYSVQAPGEIPYDGIYYDPEEVKYVF
RHAQPERPKSLRIYSTHVGMSSPEPKINTYVWRFDEYLPRIKKIGYNAVQIMAIQEHS
YYGSFGYHVTNFFAPSSRFGTPEELKSLIDRAHELGLLVLMDVYHSHASSNTLDGLNG
EDGTDTHYEHSGAPGHHWMDDSRLFNYGNWEYLRFLLSNARWHLEEYKFDGFREDGVT
SMMYTHHGLQVTFTGNENEYFGFATDVDAVVYLMLVNDLIHGLYPEAVTIGEDVSGMP
TFALFVHDGGYGFDYRHMAVADKWIDLLKQSDETWKMGDIVHTTMNRKEKCYTYA
ESHDQALVGDKTIAFWLMDKDMYDFMALDRFBTFIDRGIALHKMIRLITWGLGGEGY
LNEMGNEEFGHEWIDFPRGPQRLPSGKFIPGNNSYDKCRRFDLGDADYLRYHGMQE
EDQAAVGLLEGGYGFMTSDHOYISRKHEEDKVIVFERGADE
EDQAAVGLLEGGYGFMTSDHOYISRHGADE
EDQAAVGLLEGGYGFMTSDHOYISRHGADE
EDQAAVGLLEGGYGFMTSDHOYISRHGADE
EDQAAVGLLEGGYGFMTSDHOYISRHGADE
ENGANGERFHTSDHOYISRHGADE
ENGANGERFHTS
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5089. .5131,5328. .5387,5887. .5967,6049. .6165,6733. .6816,
7592. .7713,8465. .8584,12605. .12734,12821. .12931
13080. .13208,16260. .16363,17236. .17380,17838. .17985,
18130. .18230,18457. .18534,18801. .18956,19405. .19479,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="starch branching enzyme IIb" 2965. .3064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(2965. 3176,3283. 3428,3673. 3827,4914. 5012,
5089. 5131,5328. 5387,5887. 5967,6049. 6165,6733. 6816,
7592. 7713,8465. 8584,12605. 112734,12821. 12931,
13080. 13208,16260. 16363,17236. 17380,17838. 17985,
18130. 18230,18457. 18534,18801. 18956,19405. 19479,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKPGVYKVVLDSDAGLFGGFSRIHHAAEHFTADCSHDNRPYSFSVYTPSRTCVVYAPV
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/gene="ae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="SBEIIb"
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/cultivar="B73"
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81.6%;
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Pred. No. 3.4
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3.4e-15;
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                                                                                                                                                                                                                                                                                                 Length 23449;
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                                                                                                                                                              7644
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                DEFINITION
ACCESSION
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AUTHORS
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E14723
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  KEYWORDS
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Best Local Similarity
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PD 13
PD 13
PD 24
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PD 24
PC C12R1:5
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FT Ke
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7705 AAGCTTTGGGTAATTTCAGGATCCAGTTTTGTTTTGTCT 7742
                                                                                                                                                                                                                                                                                                                                              313 caggaaccgaagataaattcatatgctaatttttagggatgaggtgttgccaagaattaaa 372
                                                                                                                                                                                                                                                TTTGGGTATCATGTTACTAACTTCTTTGC 1007
                                                                                                                                                                                                          tttgggtattcacacaatccatttttttc 461
                                                                                                                                                                                                                                                                                                                            CCGGAACCGAAGATAAACACATATGCTAATTTTAGGGATGAGGTGCTACCAAGAATTAAA 918
E14723
Rice mRNA for branchi
E14723
E14723.1 GI:5709406
JP 1998004970-A/1.
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E14724.1 GI:5709407
JP 1998004970-A/2.
Oryza sativa.
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baba, T. KAWSAKI, T. and Ichikawa, N.
NEW RICE GENE FOR STARCH-BRANCHING ENZYME
Patent: JP 1998004970-A 2 13-JAN-1998;
MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK, MITSUI PETROCHEM IND LTD
OS OFFZAS SATIVA (rice)
PN JP 1998004970-A/2
PD 11-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUN-1996 JP 1996162983
BABA TADASHI, KAWASAKI TSUTOMU, ICHIKAWA NORIO PC
15/09,A01H5/00,C07H21/04,C12N5/10,C12N9/10,(C12N15/09,
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strandedness: Double;
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1. .2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa"
/db_xref="taxon:4530"
454 c 600 g 640
                                                         for branching
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Pred. No. 1.6e-14;
0; Mismatches 25
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/clone='pRB41'
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/cultivar='Nihonbare'
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                                                         enzyme-4, complete
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Best Local Similarity
Matches 124; Conserv
    TITLE
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NEW RICE GENE FOR STARCH-BRANCHING ENZYME
L Patent: JP 1988004970-A 1 13-JAN-1998;

MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK, MI
OS OFYZA SALLVA (Fice)
PN JP 1998004970-A/1
PD 13-JAN-1998
PF 24-JUN-1998
PF 24-JUN-1996 JP 1996162983
PF 24-JUN-1996 JP 1996167803
PI BABA TADASHI, KAWASAKI TSUTOMU, ICHIKAWA
C12N15/09,A01H5/00,C07H21/04,C12N5/10,C12N9/1
C12R1:91),
CC Strandedness: Double;
CC (C12N5/10,C12R1:91), CC12N9/10,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key
FF SOUICE

FT SOUICE

Organism-Oryza sativa'
FT /Cultivar='Nihonbare'
FT /Cultivar='Nihonbare'
FT /Cultivar='Nihonbare'
FT /Cultivar='Nihonbare'
                                                                                                                                                                                                                                                                                                tttgggtattcacacaatccatttttttc 461
                                                                                                                                                                                                                                                                                                                                                      aggcttggatacaatgcagtgcagataatggcaatccaggagcattcatactatgcaagc 432
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                                                                                                                                                                                                                                                                                                                                        AAGCTTGGGTACAATGCTGTACAGATAATGGCAATCCAGGAGCACTCTTATTACGCAAGC 1265
                                                                                                       starch branching enzyme rbe4.
Oryza sativa tissue_lib:developing
Oryza sativa
                                                                                                                                                                                   AB023498 3015 bp mRNA or starch branching
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Baba, T., Kawasaki T
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Oryza sativa
Kobayashi, M. and Baba,
Molecular cloning and
                                                            Spermatophyta;
Ehrhartoideae;
                                                                          Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                     AB023498.1 GI:5689137
                                                                                                                                                                      AB023498
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                                              (sites)
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.5/09,A01H5/00,C07H21/04,C12N5/10,C12N9/10,(C12N15/09,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
/db_xref="taxon:4530"
606 c 819 g 79,
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                                                             Oryzeae; Oryza.
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cDNA library'
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/clone='pRB41'
129. .2654
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 109; DB 6;
Pred. No. 1.6e-14;
0; Mismatches 25
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/cultivar='Nihonbare'
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   expression
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   analysis
                                                                                                                        seeds cDNA to mRNA.
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                              Kawasaki,T.,
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                               Funane, K.,
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    member
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REFERENCE
AUTHORS
TITLE
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ZMU65948
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Best Local S
Matches 124
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                                                                                                                                                                                                                                                               tttgggtattcacacaatccatttttttc 461
                                                                                                                                                                                                                                                                                                        AAGCTTGGGTACAATGCTGTACAGATAATGGCAATCCAGGAGCACTCTTATTACGCAAGC
 Gao,
                                                                                                                      Zea mays starch branching U65948 U65948.1 GI:2340107
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Mizuno, K. and Baba, T.
Direct Submission
                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                             Zea mays
                                                                                            Zea mays
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               (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        796
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Fisher,D.K.,
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129. .2654
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   Kim, K.N.,
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Pred. No. 1.6e-14;
0; Mismatches 25;
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Length 3015;

Indels

0;

Gaps

0

1265

2795 bp ng enzyme

IIa (Sbe2a) mRNA, mRNA

linear

PLN 21-AUG-1997 partial cds.

Shannon, J.C.

and Guiltinan, M.J

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Submitted (09-FEB-1999) Kouichi Mizuno, University of Tsukuba, Institute of Agricultural and Forest Engineering; 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8672, Japan (E-mail:koumno@sakura.cc.tsukuba.ac.jp, Tel:81-298-53-4656, Fax:81-298-55-2203)
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                       /product="starch branching enzyme rbe4"
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/db_xref="GI:5689138"
/db_xref="GI:5689138"
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EIPAVAEASIKVVAEDKLESSEVIQDIEENVTEGVIKDADEPTVEDKERVIFPAGGG
KIYQIDPMLEGFRNHLDYRYSEVKTMENAUGHSGLFTKAEFGIFV
REWAPGAGSAALVGDERNWNDRADSTWERNEYGVWEISLPNNADGSPAIPGFSSEVIRM
DTPSGVKDSIPAWIKFAVQAPGEIPYNGIYYDPPEEEKVVFQHPQPKRPNSLRIYESH
IGMSSPEPKINTYANFRDEVLPRIKKLGYNAVQIMAIQEHSYYASFGYHVTNFFAPSS
                                                                                                                                             RFGTPEDLKSLIDKAHELGLLVLMDIVHSHASNNTLDGLNGFDGTDTHYFHGGPRGHH
MMMDSRLFNYGSMEVLRYLLSNARMWLEBYKFDGFPDGVTSMMYTHHGLQVAFFGNY
GEYFGFATDVDAVYYLMLVNDLIHGLYPEAVALIGEDVSGMPTFCIPVODGGVGFDYRL
HMAVPDKWIELLKQSDEYMKMGDIVHTLTNRRWSEKCVTYAESHDQALVGDKTIAFWL
MDKDMYDFMALDRPSTPRIDRGIALHKMIRLVTMGLGGEGYLNEMGNEFGHPEWIDFP
                                        EHQYISRKHEEDKVIIFERGDLVFVFNFHWSNSYFDYRVGCLKPGKYKIVLDSDDGLF
GGFSRLDHDAEYFTADWPHDNRPCSFSVYTPSRTAVVYALTED"
                                                                                                                     {	t RGPQSLPNGSVLPGNNYSFDKCRRRFDLGDADYLRYHGMQEFDQAMQHLEEKYGFMTS}
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/db_xref="taxon:4530"
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Search completed: September 12, 2002, 07:29:49 Job time: 20777 sec
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Best Local Similarity 81.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 caggaaccgaagataaattcatatgctaattttagggatgaggtgttgccaagaattaaa 372
                                                                                                                                                                                                       TTTGGGTACCATGTTACGAATTTTTTGC 1077
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Submitted (02-AUG-1996) Hort./Biotech.Inst., Penn State University, 519 Wartik, University Park, PA 16802, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Independent genetic control of maize starch-branching enzymes IIa and IIb. Isolation and characterization of a Sbe2a cDNA Plant Physiol. 114 (1), 69-78 (1997) 97303618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 2795)
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VDTQPEDLQ I PEAELTYEKTSSEPTQTTSSAEPV
VDTQPEDLQ I PEAELTYEKTSSSPTQTTSAVAEASSCVAEERFELSEVIGVGGTGGT
KIDGAGI KAKARLVEEKPRVL PPGDGQR I VEI DPMLEGFEGHLDYRYSEVKRLRAD
DQHEGGLDAFSRGYEKLGFTRSAEG I TYREWAPGAYSAALVGDFNUWNPNADAMARNE
TGVWELFLPNNADGSPALPHGSRVK I RWDTPSGVWGSI I PAWIKESVQAPGEI PYNGIY
YDPPEEKYVFWKHOPGYRSAEVKI RWDTPSGVWGSI I PAWIKESVQAPGEI PYNGIY
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ADYLRYRGMQEFDQAMQHLEGKYEFMTSDHSYVSRKHEEDKVIIFERGDLVFVFNFHW
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starch biosynthesis"
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/protein_id="AAB67316.1"
/db_xref="GI:2340108"
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/db_xref="taxon:4577"
/note="inbred"
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/EC_number="2.4.1.18"
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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length: 2000000000
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1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

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3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

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        (CSIR ) COMMONWEALTH SCI & IND RES ORG. (GOOD-) GOODMAN FIELDER LITD. (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD. (AUSU ) UNIV AUSTRALIAN NAT.
                                                                     20-MAR-1998;
12-SEP-1997;
                                                                                                                                                                                                                                                                       Starch branching enzyme II (SBE II) gene sequence
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                                                                                                      11-SEP-1998;
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tgttccaggtaccatgttactaatttttttgcaccaagtagccgttttggaactccagag
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                                              altering thei
biosynthetic
produced in t
                                                                     The present sequence encodes a wheat starch branching enzyme of Aegilops tauschii, designated F2. A. tauschii is likely to be the ancestral D genome donor of wheat. Probes isolated from the present sequence were used to identify type II starch branching enzymes (SBI in wheat, especially BEIID. The BEIID nucleic acids may be used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose
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RESULT
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Best Local Similarity
Matches 141; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes wheat starch branching enzyme 9, designated BEIIa. The specification describes BEIIb. BEIIb is a type II starch branching enzyme (SBE). The BEIIb nucleic acids ne used to genetically transform cereal plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin ar amylose produced in the plant.
                                                                                                                                                                                         1159
                                                                                                                                                                                                                                                                                   1099
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                                                                      AAH78343 standard;
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(GOOD-) GOODMAN FIELDER LTD.
(LIMA-) GRP LIMAGRAIN PACIFIC
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                                                                      8381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 124.2; DB Pred. No. 2.1e-21 0; Mismatches 2
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Best Local S
Matches 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g. wheat and barley - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wheat;
starch
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          Maize amylose-extender (Ae) gene encoding starch branching enzyme
                                                   AAZ35393;
                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                          biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the plant.
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                                                                     AAZ35393 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         6;
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biosynthetic pathway; amylopectin; amylose; ss
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GOODMAN FIELDER LTD.
GRP LIMAGRAIN PACIFIC PTY LTD.
                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                       8381 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 95-98; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rahman S;
                                                                                                                                                                                                                                                                                    Conservative
                              (first entry)
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                                                                      DNA;
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                                                                      23449
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                                                                                                                                                          밁
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 129; Conserv
                                                                                                               Rice type IV starch branching enzyme cDNA
                                                                                                                                                                                                 7585 tgattaggaaccgaagataaacacatatgtaaactttagggatgaagtcctcccaagaat 7644
                                                                                                                                                                                                                                                                                              New gene regulatory sequences from plants used to provide resistance microbial path pathogens - \,
                   01-MAY-1998 (first entry)
                                         AAV05639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                             AAV05639 standard;
                                                                                                                                                         7645 aaaaaaacttggatacaatgcagtgcaaataatggcaatccaagagcactcatattatgg 7704
                                                                                                                                                                                                                                                                                                                              WPI; 2000-116538/10
                                                                                                                                                                                                                                                                                                                                                  Guiltinan MJ,
                                                                                                                                                                                                                                                                                                                                                                                            12-JUN-1998;
12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                       (UYPE-) UNIV PENNSYLVANIA STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intron
                                                                                                                                                                     369 taaaaggcttggatacaatgcagtgcagataatggcaatccaggagcattcatactatgc 428
                                                                                                                                                                                                            309 tgcacaggaaccgaagataaattcatatgctaattttagggatgaggtgttgccaagaat 368
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                            98US-0089049.
98US-0089050.
                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US13266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= au
/number= 1854
/*tag= av
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18535.18800
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18601.18956
/*tag= ax
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/number= 21
19480.19576.19659
/*tag= az
/number= 21
19480.19576.19659
/*tag= bc
/number= 21
19483.1949
/*tag= bc
/number= 23
/number= 21
/*tag= bc
                                                             cDNA to mRNA; 3015
                                                                                                                                                                                                                                                       11.1%;
81.6%;
                                                                                                                                                                                                                                            Score 111.6; DB 21;
pred. No. 5.8e-18;
0; Mismatches 29;
                                                             ВP
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                 23449
                                                                                                                                                                                                                                            0; Gaps
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5388..5886 /*tag= w /number= 6 5887..5967 /*tag= x

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12735..12820
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/number= 12
12821..12931
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13090..16363
/*tag= am
/number= 14
13630..16363
/*tag= am
/number= 14
13630..16363
/*tag= am
/number= 14
16260..16363

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sequence

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Xaa Xaa Xaa Xaa

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AAZ99938
XX
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AC AAZ9
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AC AAZ9
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DT 25-J
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DE DNA
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UNea
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Whea
KW gela
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FH Key
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                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 124
                                                                                                                                                                                                                                                                                                                               1266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes the rice type IV starch branching enzyme, which has the ability to synthesise amylopectin. The quality of starch is improved by the use of the protein.
                                         Triticum
                                                                        Wheat; starch branchi gelatinisation onset;
                                                                                                                             DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Pages 5-8; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice starch branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                  25-JUL-2000
                                                                                                                                                                                                        AAZ99938;
                                                                                                                                                                                                                                       AAZ99938 standard; DNA; 2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                high quality starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-133625/13.
P-PSDB; AAW41763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP10004970-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MITS-) MITSUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313
                                                                                                                                                                                                                                                                                                                                                                   433
                                                                                                                                                                                                                                                                                                                                                                                                                                        373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caggaaccgaagataaattcatatgctaattttagggatgaggtgttgccaagaattaaa 372
                                                                                                                                                                                                                                                                                                                              tttgggtatcatgttactaacttctttgc 1294
                                                                                                                                                                                                                                                                                                                                                               tttgggtattcacacaatccattttttc 461
                                                                                                                                                                                                                                                                                                                                                                                                   aagcttgggtacaatgctgtacagataatggcaatccaggagcactcttattacgcaagc
                                                                                                                                                                                                                                                                                                                                                                                                                  aggcttggatacaatgcagtgcagataatggcaatccaggagcattcatactatgcaagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ccggaaccgaagataaacacatatgctaattttagggatgaggtgctaccaagaattaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                               part of
                                                                                                                                                               (first entry)
                                                         branching enzyme 11; Speri, Conset; transgenic plant; foodstuff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        starch branching enzyme; amylopectin synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYOSAI SHOKUBUTSU BIO KENKYUSHO. TOATSU CHEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96JP-0162983
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288..2651
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129..287
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.9%;
                                                                                                                           starch branching enzyme II clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; 606 C; 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         type_IV_starch_branching_enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 109; DB Pred. No. 1.4e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>ი</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthesises amylopectin to yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
.4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                   starch;
bakery product;
                                                                                                                             5A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                   1265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1205
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Qy
                                     뫄
                                                                   QΨ
                                                                                                          망
                                                                                                                                            QΥ
                                                                                                                                                                                   В
                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 157
                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a wheat starch branching enzyme II (SBEII) of a novel subclass of known SBEII genes, designated SBEII-1. The SBEII-1 genes are thought to have similar functional properties to the maize SBEIIb gene. Starch branching enzymes catalyse the formation of the alpha-1,6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed by reattachment of the released alpha-1,4-9 lucan chain to the same or another glucosyl chain. SBEII polypeptides can be used to alter the characteristics of a plant, in particular to alter starch so that it has an elevated gelatinisation onset and/or peak temperature. Starch obtained from transgenic plants is useful in the preparation or processing a foodstuff, particularly bakery products.
                                                                                                                                                                                                                                                                                                                                             Sequence 2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starc gelatinization onset and/or peak temperature -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 10; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-271446/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goldsbrough A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PLAN-) PLANT BREEDING INT CAMBRIDGE
                                     344
                                                                                                                                                                                   228
                                                                        340
                                                                                                                                                280
                                                                                                                                                                                                                     220
400 atggcaatccaggagcattcatactatgcaagctttgggta 440
                                                                                                          284 cggatatatgaaacacatgttggcatgagtagcccggaaccaaagatcaacacatatgca 343
                                                                                                                                                                                                                                                      Local Similarity
mes 157; Conser
                                                                                                                                                                                                    cctacttggaaacttgagtcttgaggcatcgctaatatatactatcatcacaatacttag 279
                                   aacttcagggatgaggtgcttccaagaattaaaagacttggatacaatgcagtgcaaata
                                                      aattttagggatgaggtgttgccaagaattaaaaggcttggatacaatgcagtgcagata
                                                                                                                         aggatgcatctgaaattttagtgtgatcttgcacaggaaccgaagataaattcatatgct 339
                                                                                                                                                                               ccgaagaggagaagtatgtattcaagcatcctcaacctaaacgacca----aaatcattg 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY84408.
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                              BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98EP-0307337.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colliver
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/*tag=
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/product= "starch
/transl_except= (F
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                                                                                                                                                                                                                                                                                                                                              674 A; 440 C;
                                                                                                                                                                                                                                                                         10.7%;
                                                                                                                                                                                                                                                                       .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Xaa is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   termination codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contains 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŝ
                                                                                                                                                                                                                                                     Score 107; DB 21;
Pred. No. 4.2e-17;
0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (pos:
                                                                                                                                                                                                                                                                                                                                              544 G; 635 T; 14 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (pos:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (pos:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2036 . 2038 aa : 2053 aa : 2051 . 2053 aa : 2050 . 2098 aa : 2114 . 2116 aa : 2117 . 2119 . aa : 2117 . 2129 . aa : 2117 . 2127 aa : 2117 . 2117 . aa : 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzyme
                                                                                                                                                                                                                                                        60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid;
                                                                                                                                                                                                                                                                                        Length 2307;
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codons,
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밁
                                                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                The present sequence encodes a wheat starch branching enzyme, designated BEIIb. BEIID is a type II starch branching enzyme (SBE The BEIID nucleic acids may be used to genetically transform cere: plants such as wheat or barley and for altering their nutritional content by modulating the starch biosynthetic pathway to vary lev of amylopectin and/or amylose produced in the plant.
 1277
                                          1217
                                                                                    1157
                                                                                                                              1101
                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding wheat starch branching enzyme IIb, useful for altering the amylose and amylopectin content of cereal plants, e.g.
                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200162934-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wheat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH78342 standard;
                                                                                                                                                                                                                             Sequence 2968 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                 Morell M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2001; 2001WO-AU00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH78342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CSIR )
                                                                                                                                         (GOOD-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aggatgcatctgaaattttagtgtgatcttgcacaggaaccgaagataaattcatatgct
       atggcaatccaggagcattcatactatgcaagctttgggta 440
                                                     aattttagggatgaggtgttgccaagaattaaaaggcttggatacaatgcagtgcagata
                                                                                   cggatatatgaaacacatgttggcatgagtagcccggaaccaaagatcaacacatatgca
                                                                                                                             ccgaagaggagaagtatgtattcaagcatcctcaacctaaacgacca----aaatcattg
                                        aacttcagggatgaggtgcttccaagaattaaaagacttggatacaatgcagtgcaaata
                                                                                                                                                                                                                                                                                                                                                                                             2001-570635/64.
                                                                                                                                                                        156;
                                                                                                                                                                                                                                                                                                                            6; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        starch branching enzyme; BEIIb; SBE; transg-
biosynthetic pathway; amylopectin; amylose;
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMONWEALTH SCI & IND GOODMAN FIELDER LID. GRP LIMAGRAIN PACIFIC P
                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  Rahman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                            9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                            103pp;
                                                                                                                                                                                                                             784 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                   10.5%;
                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                             626 C;
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                                                                                                                                                                        0;
                                                                                                                                                                        Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                   Score 105.4; DI
Pred. No. 1.1e-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enzyme
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                                                                                                                                                                         Indels
                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                             vary levels
                                                                                                                                                                                             2968;
                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                   cereal
                                                                                                                                                                                                                                                                                             (SBE).
                                                                                                                                                                        Gaps
                                                                                   1216
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AAT69737
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Best Local S
Matches 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A cDNA insert (AAT69737) in plasmid pBE96 comprises a 2.09 kb fragment of corn starch branching enzyme IIb (SBEIIb) cDNA (see also AAT69729), starting at the initiating ATG codon of the codir region and terminating 312 bp 5' of the translation termination codon. It was obtd. by site-specific mutagenesis of the SBEIIb gene in plasmid pBE240 to generate an NCOI site at the ATG start site, and EcoRI digestion of the mutagenised plasmid. The 2.09 kb fragment was inserted, in sense orientation, between the zein promoter and 3' regions in vector pMIO3 to produce pBE96. Co-suppression and antisense techniques can be used to inhibit SBEIIb in transgenic plants and thereby alter starch properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corn starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT69737 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic cocontrolled -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Broglie KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09722703-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Starch branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UD ( OPUC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-DEC-1996;
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                                                                                                                                                                                                        827
                                                  365
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                                                                                                                                                                                                                                                        245
                                                                                                                                                                                                                                                                                                          767
                                                                                                                                                                                                                                                                                                                                                             187
                                                                                                                                                                                                                                                                                                                                                                                                                707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 57.
les 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        gaattaaaaggcttggatacaatgcagtgcagataatggcaatccagggagcattcatact 424
gaataaaaaaacttggatacaatgcagtgcaaataatggcaatccaagagcactcatatt
                                                                                                                             atcttgcacaggaaccgaagataaattcatatgctaattttagggatgaggtgttgccaa
                                                                                                                                                                                                     tcaggcatgcgcaacctaaacgaccaaaatcattgcggatatatgaaacacatgtcggaa
                                                                                                                                                                                                                                  caggagaaataccatatgatgggatttattatgatcctcctgaagaggtaaagtatgtgt 826
                                                                                                                                                                                                                                                                                                                                        atactccatcagggataaaggattcaattccagcctggatcaagtactcagtgcaggccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1997-341694/31.
                                                                                                  tgagtagcccggaaccgaagataaacacatatgtaaactttagggatgaagtcctcccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Page 56-57; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preparation
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    specifically branch chain distribution of amylopec
preparation of thickened foodstuff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hubbard NL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic plant; pBE96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 565 A; 396 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95us-0009113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US19678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.1%; 57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pred. No. 1.5e.
O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIb gene fragment in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                573 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           рвЕ96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amylopectin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                        Query Match
Best Local S
Matches 201
                                                                                                                                                                                                                                                                                                       A 2.16 kb cDNA insert (AAT69736) in plasmid pBE45 comprises the entire 5' untranslated region as well as 2.08 kb of the coding region of corn starch branching enzyme IIb (SBEIIb) cDNA (see also AAT69729). It was generated by EccRI digestion of plasmid pBE240 and was inserted into vector pML103 in antisense orientation with respect to a maize 27 kba zein promoter and a 10 kba zein gene 3' sequence. Transgenic corn plants expressing the near full-length SBEIIb antisense transcript demonstrated a unique starch
 1201
                                                    1261
                                                                                                                                                        1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Starch branching enzyme amylopectin; transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1007
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic corn in which grain derived starch fine structure is controlled - specifically branch chain distribution of amylopectin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corn starch branching enzyme
                                                                                                                                                                                                                                                                                              branching phenotype.
                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful in preparation of thickened foodstuff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-341694/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DUPO ) DU
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                                                                          245
                                                                                                                               187
                                                                                                                                                                                127
                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                       ATACTCCATCAGGGATAAAGGATTCAATTCCAGCCTGGATCAAGTACTCAGTGCAGGCCC
                                                                                                                                                                            attotgogagogattoaaaaacttocattgttotgaggtgtacgtactgcagggatotco
TGAGTAGCCCGGAACCGAAGATAAACACATATGTAAACTTTAGGGATGAAGTCCTCCCAA
                                                                 atcttgcacaggaaccgaagataaattcatatgctaattttagggatgaggtgttgccaa 364
                                                  TCAGGCATGCGCAACCTAAACGACCAAAATCATTGCGGATATATGAAACACATGTCGGAA
                                                                                                     CAGGAGAAATACCATATGATGGGATTTATTATGATCCTCCTGAAGAGGTAAAGTATGTGT
                                                                                                                            cattatgaagaggatat--agttaattctttgtaacctacttggaaacttgagtcttgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atggaagctttggataccatgtaactaatttttttgcgccaagtagtcgt
                                                                                                                                                                                                        201;
                                                                                                                                                                                                                                                                       2165 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                         Page 55-56; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PONT
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hubbard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US19678
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                                                                                                                                                                                                                                                                       593 A; 580 C; 416 G;
                                                                                                                                                                                                                   10.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIb; SB
plant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SBEIIb; ot; pBE45;
                                                                                                                                                                                                        Score 100.8; DE
Pred. No. 1.5e-1
0; Mismatches 1
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                                                                                                                                                                                                                                                                       576
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                                                                                                                                                                                                                               DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        maize; antisense;
                                                                                                                                                                                                        147;
                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pBE45
                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                  2165;
                                                                                                                                                                                                        2
                                                                                                                                                                                                       Gaps
                                                                                                    1262
                                                                                                                             244
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                                                                                                                                                                               186
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                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing non-glycogen-like polysaccharides in bacteria, fungi plants - transformed with genes for enzymes involved in starch glycogen synthesis allows fermentative production of starches we engineered properties
                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                        new starches in plants. These stanon-food applications of starch. the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The specification describes a method for the production of non-glycogen-like polysaccharides in a host. The method comprises transforming a host, suitable for fermentation, with genes encoding starch- or glycogen-synthesis enzymes, and fermenting the transformant starch- or glycogen synthesis enzymes, and fermenting the transformant starch- or glycogen synthesis enzymes, and fermenting the transformant starch- or glycogen synthesis enzymes, and fermenting the transformation also describes hosts transformed with a gene active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 53; 150pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-starch branching gene; amy
maize branching enzyme II; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-glycogen-like polysaccharide production; ferment starch synthesis enzyme; glycogen-synthesis enzyme; non-starch branching gene; amylopectin; amylose; planting the starch branching gene; amylopectin; amylose; planting gene; amylopectin; amy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                  in glycogen synthesis and at least one non-starch branching gene, involved in production of amylopectin or amylose in its original host. The method is used to produce plant-like starches by fermentation and new starches in plants. These starches are useful for all food and non-food applications of starch. The present sequence is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
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DB; AAW70895.
                                                                                atactccatcagggataaaggattcaattccagcctggatcaagtactcagtgcaggccc 771
cattatgaagaggatat--agttaattctttgtaacctacttggaaacttgagtcttgag
                                                                                                                     atycaayctttyyytattcacacaatccatttttttctytatacactctt
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                                                                                                                                                                                                                          Similarity
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Pred. No. 1.6e-1
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                                               A cDNA insert (AAT69729) in plasmid clone pBE240 comprises a EcoRI-XhoI fragment isolated from a corn cDNA library. It in an open reading frame encoding starch branching enzyme IIb (S (AAW19212). The insert was used as a starting point in the a of DNA constructs (see also AAT69730, AAT69736-37) designed the achieve suppression of SBEIIb expression in transgenic corn pand thereby to produce novel starches that have properties beneficial in food and industrial applications.
                                                                                                                                                                                                                                                                                                             Transgenic corn in which grain derived starch fine structure is controlled - specifically branch chain distribution of amylopectin, useful in preparation of thickened foodstuff
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Broglie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Starch branching enzyme IIb; SBEIIb; corn; amylopectin; transgenic plant; pBE240; ss.
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DB; AAW19212.
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Query Match Best Local Similarity

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Score Pred.

100.8; DB 18; No. 1.6e-15;

Length

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                                 Hybrid polypeptide comprising starch-encapsulating protein - useful for, e.g. producing protein(s) redegradation by stomach acids
                                                                                 WPI; 1998-240100/21.
                                                                                                   Guan H,
                                                                                                                                                                                                                          mat_peptide
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                                                                         P-PSDB;
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                Example 2; Page 44; 156pp; English.
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265..2487
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                                                                                                                                                                                                                                                                                                                                                                       entry
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                                                                                                                      FIC
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising a starch-encapsulating region (SER) fused to a payload protein. The hybrid polypeptide can be used to make modified starches comprising the payload protein, selected from, e.g. hormones, growth factors, antibodies, enzymes, dyes, immunoglobulins, etc. The modified starch can also be used to provide grain feeds enriched in amino acids. By encapsulating the payload protein in starch, it is more resistant to degradation by stomach acids.
                                                                                                                                                                                                                                                                                                                                                                                      1097
                                                                                                                                                                                                                                                                                                                                                                                                                                   1037
                                                                                                                                                                        5'UTR
                                                                                         3'UTR
                                                                                                                          mat_peptide
                                                                                                                                                                                                                                Starch branching enzyme; rice;
                                                                                                                                                                                                                                                      Rice starch branching enzyme
                                                                                                                                                                                                                                                                                05-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
         22-OCT-1993;
                                20-SEP-1994
                                                      JP06261767-A
                                                                                                                                                 transit_peptide
                                                                                                                                                                                    Key
                                                                                                                                                                                                         Oryza sativa
                                                                                                                                                                                                                                                                                                       AAQ73750;
                                                                                                                                                                                                                                                                                                                             AAQ73750 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           It can be used in the production of a hybrid polypeptide
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                                                                                                                                                                                                                                                                              (first entry)
         93JP-0265171
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323..2606
                                                                             /product= branching_enzyme
2603..2919
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                                                                                                                                                                                                                                starch content; ds
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RESULT 1
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Best Local S
Matches 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The rice starch branching enzyme is encoded by the cDNA sequence AAQ73750. The starch content of rice grains can be increased by increasing the expression of branching enzyme in rice plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-337418/42
                                                                                                                                                                                                                                      Starch branching enzyme;
                                                                                                                                                                                                                                                        cDNA encoding
                                                                                                                                                                                                                                                                                                              AAV38722 standard; DNA; 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New gene of branching enzyme of rice starch - increasing starch yield of rice grains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR60811.
                 P-PSDB; AAW62650
                                                                               05-NOV-1996;
                                                                                                                                                                                                                                                                                             AAV38722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MITS-) MITSUI GYOSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1992;
                         WPI; 1998-286958/25
                                                                                                 04-NOV-1997;
                                                                                                                   14-MAY-1998
                                                                                                                                    WO9820145-A2
                                                                                                                                                                                                                     Manihot esculenta.
                                                                                                                                                                                                                                                                           21-SEP-1998
                                          Jobling SA,
                                                             (NATT )
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                                                                                                                                                                                                                                                                                                                                                                          tgggtattcacacaatccatttttttctgtatacactctt 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121;
                                                             NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 9-12;
                                                             STARCH & CHEM INVESTMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                           (first entry)
                                           Safford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP;
                                                                                                                                                                                                                                                        starch branching enzyne II (SBE
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                                                                                96GB-0023095
                                                                                                  97WO-GB03032
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/product= SBE 1
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                                                                                                                                                                                                                                       SBE; cassava;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                              HOLDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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0,

Starch branching gene from

cassava

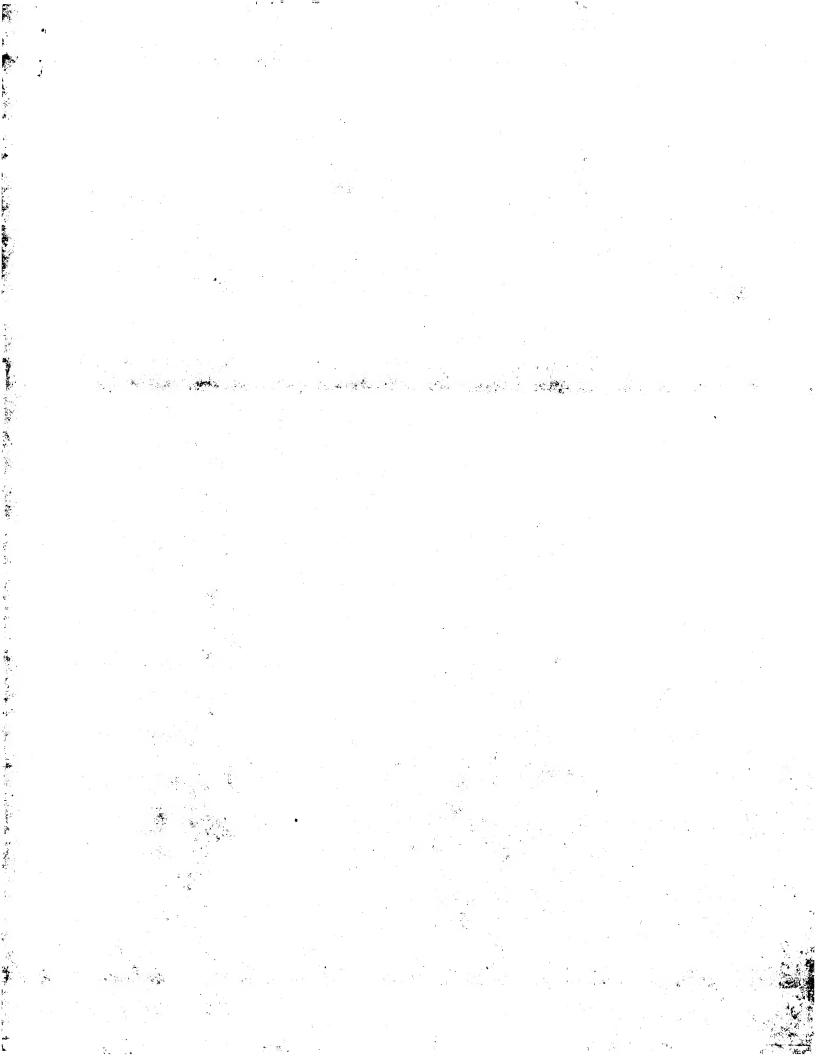
useful

for

producing altered

plants giving modified starch

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Search completed: September 12, 2002, 08:21:51 Job time: 12268 sec
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                                                                                                                                                                                     Вb
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                                                                                                                                                                                                                                                                                                                        SXCCCCCXXXX
                                                                                                                                                                                                                                               Query Match 9.5%;
Best Local Similarity 78.6%;
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes starch branching enzyme (SBE) II. It was isolated from cassava tubers. The products can be used for producing plants having altered starch quantities and qualities. They can also be used for producing altered plants such as cassava, banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato and rice plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Fig 10; 67pp; English.
                                                                                                                                                                                                                                                                                                                       Sequence 1919 BP; 543 A; 324 C; 467 G; 585 T; 0 other;
                                                                                                                           164
                                                                                     704 ttgttcttatggatattgttcatag 728
                                                                      ttgttctcatggatattgttcatag 188
                                                                                                                                                                                                                                              Score 95.4; DB 19; Length 1919;
Pred. No. 3.2e-14;
0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                 0;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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71.2
63.4
63.4
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length: 2000000000
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1: /cgn2_6/ptodata/1
2: /dgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
4: /cgn2_6/ptodata/1
5: /dgn2_6/ptodata/1
6: /cgn2_6/ptodata/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match Length
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383533 seqs, 122816752 residues
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Packfiles1.seq:*
                      111478
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              US-08-941-445h-14
US-09-087-277-1
US-09-087-277-1
US-09-087-277-1
US-08-981-803-29
US-08-983-440-29
US-08-9104-158-1
US-08-9165-315D-2
US-08-165-315D-2
US-08-165-315D-2
US-08-165-315D-3
US-08-165-315D-3
US-08-165-315D-3
US-08-165-315D-3
US-08-165-315D-3
US-08-165-315D-3
US-08-165-315D-3
US-08-165-315D-3
US-08-165-193B-1
US-08-165-193B-1
US-08-645-193B-1
US-08-232-463-1
US-09-172-339-3
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Compugen Ltd.
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2649.845 Million cell updates/sec
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-416-	4	663		33.4	40	
-416-	4	662		Ψ	39	O
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-242-690A	4	1680		ω	37	
-17	N	1185		ω.	36	O
US-07-861-458C-	4	4093		ω	ω 5	
US-09-266-417-5	4	398		Ψ	34	O
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8-416-	4	854		34	30	
5-136-	4	8133		4	29	
5-49	N	8133		4	28	
	-08-405-4 -08-915-1 -08-918-4 -08-998-4 -08-98-4 -09-265-3 -09-265-3 -09-265-3 -09-265-4 -07-861-4 -08-998-4 -08-998-4 -08-998-4 -08-998-4 -08-998-4 -08-998-4 -08-998-4 -08-998-4	-08-40: -08-91: -08-91: -08-91: -08-91: -09-26: -09-26: -09-26: -09-26: -09-26: -09-26: -09-26: -09-26: -09-26: -09-26: -09-26: -09-24: -09-24: -09-24: -09-24: -09-24: -09-24: -09-24: -09-24: -09-24: -09-24: -09-24: -09-24: -09-29: -08-99	US-08-40: US-08-91: US-08-92: US-09-26: US-09-26: US-09-26: US-09-26: US-09-26: US-09-26: US-08-99: US-08-	33 2 US-08-401 33 4 US-08-911 54 4 US-08-991 98 4 US-09-26 98 4 US-09-26 98 4 US-09-26 98 4 US-09-26 99 4 US-09-26 10 US-09-24 11 4 US-08-99 12 4 US-08-99 13 4 US-08-99 14 US-08-99 15 4 US-08-99 16 5 4 US-08-99 17 4 US-08-99 18 5 4 US-08-99 18 6 5 4 US-08-99	2 3.4 8133 2 US-08-40; 2 3.4 8133 4 US-08-9; 4 3.4 854 4 US-08-99; 4 3.4 398 4 US-09-26; 8 3.4 398 4 US-09-26; 8 3.4 398 4 US-09-26; 8 3.4 1185 2 US-08-17; 6 3.4 1185 2 US-08-19; 4 3.3 663 4 US-09-24; 4 3.3 663 4 US-08-99; 4 3.3 701 4 US-08-99; 4 3.3 724 4 US-08-99; 4 3.3 724 4 US-08-99; 4 3.3 732 4 US-08-99;	4.2 3.4 8133 2 US-08-40; 4.2 3.4 8133 4 US-08-9; 34 3.4 854 4 US-08-99; 3.8 3.4 398 3 US-08-71; 3.8 3.4 398 4 US-09-26; 3.8 3.4 398 4 US-09-26; 3.8 3.4 4093 4 US-09-26; 3.6 3.4 1185 2 US-08-17; 3.6 3.4 1185 2 US-08-17; 3.6 3.4 1185 2 US-08-17; 3.6 3.4 1185 2 US-08-9; 3.4 3.3 662 4 US-08-99; 3.4 3.3 701 4 US-08-99; 3.4 3.3 701 4 US-08-99; 3.4 3.3 772 4 US-08-99;

5, Appli 534, App 534, Appli 5, Appli 5, Appli 5, Appli 5, Appli 1, Appli 14, Appli 114, Appli 117, Appli 118, Appli 119, Appli 119,

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US-08-941-445A-14
                                                                                                                                                                                                                                         MEDIUM TYPE: FLUPPY CLAR
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers:
SOFTWARE: Patentin Release #1.0, Vers:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
FENCTH: 2725 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08941445A Patent No. 6107060 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
                                                                                 FEATURE:
                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                         MOLECULE TYPE: mI
                                         NAME/KEY:
LOCATION:
                                                                                                                                                                               LENGTH: 2725 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 5370 P
CITY: Boulder
                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 80303
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    NAME/KEY:
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                                         sig_peptide
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TITLE OF INVENTION: STARCH BRANCHING ENZYME II FILE REFERENCE: 003300-486

CURRENT APPLICATION NUMBER: US/09/087,2778

CURRENT FILING DATE: 1998-05-29

EARLIER APPLICATION NUMBER: PCT/SE96/01558

EARLIER APPLICATION NUMBER: PCT/SE96/01558

EARLIER APPLICATION NUMBER: SE 9504272-7

EARLIER FILING DATE: 1995-11-29

EARLIER APPLICATION NUMBER: SE 9501506-0

EARLIER FILING DATE: 1995-04-19

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.0
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US-09-087-277-1
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Best Local Sin
Matches 201;
                                                                                                                                                                                                                      SEQ ID NO 1
LENGTH: 3074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence 1, Application US/09087277B Patent No. 6169226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: EK, BO
APPLICANT: KHOSNOODI,
                                                        FEATURE:
NAME/KEY: CDS
LOCATION: (189)...(2825)
         NAME/KEY: sig_peptide
LOCATION: (189)..(332)
                                                                                                              OTHER INFORMATION: Description of Unknown OTHER INFORMATION: (branching enzyme II) forther information: (potato)
FEATURE:
                                                                                                                                                                     FEATURE:
                                                                                                                                                                                   ORGANISM: Unknown
                                                 FEATURE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atcttgcacaggaaccgaagataaattcatatgctaattttagggatgaggtgttgccaa 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGAGAAATACCATATGATGGGATTTATTATGATCCTCCTGAAGAGGTAAAGTATGTGT 916
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57.4%;
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                                                                                                                                Organism:beII gene
from Solanum tuberosum
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CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EEARLIER APPLICATION NUMBER: PCT/SE96/0158
EEARLIER FILING DATE: 1996-11-28
EEARLIER FILING DATE: 1996-11-28
EEARLIER FILING DATE: 1995-11-29
EEARLIER FILING DATE: 1995-11-29
EEARLIER APPLICATION NUMBER: SE 9601506-0
EEARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO SEQ ID NOS: 4
SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                  US-09-087-277-3
                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application Patent No. 6169226 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.8%;
Best Local Similarity 73.0%;
Matches 111; Conservative
                                                                                                                                                                                                               APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME
FILE REFERENCE: 003300-486
                                                                                                                                                                                                                                                                                                         APPLICANT: EK, BO APPLICANT: KHOSNOODI,
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotide
OTHER INFORMATION: n wherein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1896)..(1898)
OTHER INFORMATION: Amino acid
OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: (1428)..(1430) OTHER INFORMATION: Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: (1404)..(1406) OTHER INFORMATION: Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: (285)..(287) OTHER INFORMATION: Ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: mat_peptide LOCATION: (333)..(2825)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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||||||||||| | | | | | | | | 1111
1494 attgttcacagccatgcatcaaataattacttt 1525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1374 gctagttttggttatcatgtcacaaattttttngcaccaagcagccgttttggaacnccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 gcttgttccaggtaccatgttactaatttttttgcaccaagtagccgttttggaactcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are n wherein n = A, C, G or T.
                                                                                                                                                                                                                                                                                                                                                                                   US/09087277B
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Pred. No. 3.1e-15;
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LOCATION: (422)..(424)
OTHER INFORMATION: Amino acid 141
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LOCATION: (424)..(1150)
OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n =
OTHER INFORMATION: C, G or T.
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LOCATION: (2)..(1393)
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          SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan,
STREET: 5370 Manhattan Circle
                                                                                                                                                                                                                                                                         APPLICANT: Keeling, Peter APPLICANT: Guan, Hanping TITLE OF INVENTION: Starch NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428
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                                                                                                                                                     COUNTRY: U
ZIP: 80303
CLASSIFICATION:
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Pred. No. 6.4e-15;
0; Mismatches 42
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APPLICANT: POULSEN, PETER
TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
FILE REFERENCE: 67459-2004
CURRENT APPLICATION NUMBER: US/08/981,803
CURRENT FILING DATE: 1997-04-17
EARLIER APPLICATION NUMBER: PCT/EP96/03052
EARLIER APPLICATION NUMBER: 9514435.8
EARLIER APPLICATION NUMBER: 9514435.8
EARLIER FILING DATE: 1995-07-14
NUMBER OF SEQ ID NOS: 33
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                                                               ; ORGANISM: Solanum tuberosum US-08-981-803-29
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SEQ ID NO 29
LENGTH: 11478
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Best Local Similarity
Matches 97; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 2763 base pairs
TYPE: nucleic acid
                                                                                                 TYPE: DNA
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NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,:
REFERENCE/DOCKET NUMBER:
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LOCATION:
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Score 63.4; DB 3; Pred. No. 3.3e-08;
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Query Match Best Local Similarity

Length 11478;

Matches

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; LCCATION: (1)..(11478)
; OTHER INFORMATION: M Stands for A or
US-08-983-440-29
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US-08-983-440-29
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/08/983,440 CURRENT FILING DATE: 1998-04-17 EARLIER APPLICATION NUMBER: 9514437.4 EARLIER FILING DATE: 1995-07-14 EARLIER FILING DATE: 1995-07-14 EARLIER APPLICATION NUMBER: PCT/EP96/03053 EARLIER FILING DATE: 1996-07-12 NUMBER OF SEQ ID NOS: 35
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TYPE: DNA
ORGANISM: Solanum tuberosum
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OTHER INFORMATION: W stands
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OTHER INFORMATION: K stands
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                                                                                  aatccttgatcgatagagcacatgagcttggtttgcttgttcttattggatattgttcata
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                                                                                                                                                                                                 85;
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                                                                                                                                                                                             Similarity 70.2
85; Conservative
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Pred. No. 3
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US-08-104-158-1
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APPLICANT: Willmi
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 212-382-0700
TELEFAX: 212-382-0888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP PCT/EP92/00302
FILING DATE: 11-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 41 04 782.6
FILING DATE: 13-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2909 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                      FEATURE:
                                                                                                                                      CELL TYPE: tot
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                               ANTI-SENSE: NO
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                                                              NAME/KEY:
LOCATION:
            OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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FILING DATE: 13-AUG
CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 10036-8403
                                                                                                                                                                         TISSUE TYPE:
                                                                                                                                                                          DEVELOPMENTAL STAGE: growing TISSUE TYPE: tuber
                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Meilman, Edward REGISTRATION NUMBER: (
                                                                                                                     LIBRARY:
                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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                                                                                                                       cDNA of total tuber mRNA in
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Visser, Richard Gerardus Francisus
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                                                                    2..1699
                                                                                                                                                      total tuber
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13-AUG-1993
                                                                                                                                                                                                                                                                                                  cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                     double
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CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE
CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND PLANTS CONTAINING THESE
            /note= "for Branching
(partial) truncated pu
active potato branchir
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              al) truncated prof
potato branching
                                                                                                                                                                                             tuber
                                                                                                                     pUC 19 (Hinc II)
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protein;
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Best Local S
Matches 84
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                                                                                                                                                                                                                                                                                               TELEFAX: (416) 363-7246 INFORMATION FOR SEQ ID NO:
                                                                                                                HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WORD 7.0 for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: IMB 1.44 MB High Density Diskette
COMPUTER: COMPAQ Deskpro 590 (IBM PC compatible
OPERATING SYSTEM: WINDOWS 95
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 368-2400
                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Anita E.Nador
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: National Starch and Chemical Investment
APPLICANT: Holding Corporation
TITLE OF INVENTION: Method for Producing Altered Starch
                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                               NAME: Anita E.Nador REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: POFILING DATE: 22.03.95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: FILED
                 TISSUE TYPE:
                                                                                               ORGANISM:
                                                                                                                                                                               DESCRIPTION:
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                                  HAPLOTYPE:
                                                DEVELOPMENTAL STAGE:
                                                                   INDIVIDUAL
                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84;
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TYPE:
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AL ISOLATE:
                                                                                                                                                                                                                                                              3128 base pairs
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Box 194, 24th Floor, Toronto-Dominion Bank Tower
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                                                                                               Solanum tuberosum
                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/08/716,449
FILED CONCURRENTLY HEREWITH
                                                                                                                                                                               cDNA encoding
                                                                                                                                                                                                                                 single
                                                                                                                clone 1.2.1 and
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                                                mature tuber
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Pred. No. 5.3e-08;
0; Mismatches 37;
                                                                                                                                                                               starch branching enzyme
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM: MS DO
SOFTWARE: WORD PROCESSO
CURRENT APPLICATION DATA:
                                                  REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-324-6155
                                                                                                                           FILING DATE: 2 December ATTORNEY/AGENT INFORMATION: NAME: Mary M. Krinsky
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1119 G 1119
                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1059 AGTATCTGATAGATAAAGCACATAGCTTGGGTTTACAGGTTCTGGTGGATGTAGTTCACA 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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CHROMOSOME/SEGMENT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                608 ggtaccatgttactaatttttttgcaccaagtagccgttttggaactccagaggacttaa 667
                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/165,315D FILING DATE: 10 December 1993 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD: lone ORF with homology to other IDENTIFICATION METHOD: branching enzymes OTHER INFORMATION: complements KV832 E. coli glycogen OTHER INFORMATION: branching enzyme mutant
                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Stamford
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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CLONE: 1.2.1 and E2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               986 Bedford Street
                                    201-327-1096
                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roger Kalla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Odd-Arne Olsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                           Word Processor
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                                                                                                                                                                                                                                                                                                                                                   3.5" 1.44 Mb diskette
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                                                                                          2105-P0001
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Pred. No. 5.5e-08;
0; Mismatches 37;
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MOLECULE TYPE:

TYPE: nucleic acid STRANDEDNESS: sing TOPOLOGY: linear

single

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US-08-702-609A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                        TELEFAX: 203-327-1096
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION: FRAGMENT TYPE: FEATURE:
                                                                                         SEQUENCE CHARACTERISTICS LENGTH: 807 residues TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: WINDOWS SOFTWARE: WORD PROCESSING CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
                            ORIGINAL SOURCE:
                                             MOLECULE TYPE:
                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-324-6155
                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Promoter from a Lipid TITLE OF INVENTION: Transfer Protein Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
               ORGANISM:
                                                              TOPOLOGY:
                                                                          STRANDEDNESS:
                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20-NOV-1996
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/702,609A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: N-1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Program NRC
No. 6031152way
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                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Biotechnical Sciences, Agricultural Biotechnology University of No. 6031152way and Agricultural Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Molecular Biology Laboratory,
Department of Biotechnical Sciences, Agricultural
                                             Genomic DNA
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terminal fragment
                                                                             double
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                           98
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853 tggcataaggaaaattggcaaaaactagagtggcaaaaataaaattttcc 902

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                                                                     Query Match
Best Local
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                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-324-6155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Odd-Arne Ols
APPLICANT: Roger Kalla
TITLE OF INVENTION: Pro
                                                                                                                                                                                   DESCRIPTION: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Processor CURRENT APPLICATION DATA:
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                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2 December 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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293
              793 gcaattatgatacattgtcaaaagctaagagtggcgaaagtgaaatgtcaaaatctagag 852
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                                                                    Local
                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/165,315D FILING DATE: 10 December 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
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MEDIUM TYPE: 3...
IBM PC
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                                                                                                                                                                                                                                                                       LENGTH:
GGAATGGAAATTATTTGTCAAAAACCTAAGAGTGGCAAAACTGAAAATGTCAAAACCTAGAG 234
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                                                      l Similarity
75; Conserv
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                                                                                                                                                                                                                                                                          846
                                                      Conservative
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                                                                                                                                         Ltp2 gene promoter and nucleotides GUS fusion
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FR: 2105-P0001
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                                                     Score 54; DB Pred. No. 5e-0 0; Mismatches
                                                      0;
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Pred. No. 4.9e-06;
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                                                                    DB 1;
5e-06;
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RESULT 13
US-08-565-907A-1/c
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US-08-165-315D-3/c
                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: Ltp2 gene
US-08-165-315D-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08165315D Patent No. 5525716
                                               Sequence 1, Application US/08565907A Patent No. 5814499
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 932
FILING DATE: 2 DECEMBER 19
ATTORNEY/AGENT INFORMATION:
NAME: MATY M. KILINSKY
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Process
CURRENT APPLICATION DATA:
                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-324-6155
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                                                                                                                                                                                     853 tggcataaggaaaattggcaaaaactagagtggcaaaaataaaaattttcc 902
      APPLICANT:
                                                                                                                                                                                                                                    293
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 10 Dec
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                    TGACATAAACAAAATTTACCCATCACTAAATGAGCACAAAATATTTCACC 184
                                                                                                                                                                                                                                 GGAATGGAAATTATTTGTCAAAACCTAAGAGTGGCAAAACTGAAATGTCAAAACCTAGAG 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201-327-1096
Sylvain Moineau, Barbara
J. Holler, Peter A. Vandenbergh,
Ebenezer R. Vedamuthu, Jeffrey K.
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                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                Score 54; DB 1; Length 1327; Pred. No. 6e-06;
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; PUBLICATION INFORMATION: US-08-565-907A-1
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TELEX: NO. 5814499e
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US
FILING DATE: December
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KONDO
TITLE OF INVENTION: I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
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MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: L
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (517) 347-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
                                                                                                                                            LIBRARY: genom
                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
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                                                                                                  FEATURE:
                                                                                                                   POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                           OTHER INFORMATION: OTHER INFORMATION:
                                                       NAME/KEY: phage abortive infection LOCATION: N/A IDENTIFICATION METHOD: sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 440,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 20 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                         CELL LINE:
                                                                                                                                                                                                        CELL TYPE:
                                                                                                                                                                                                                        TISSUE TYPE:
                                                                                                                                                                                                                                      HAPLOTYPE:
                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                             ORGANISM: Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE:
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                                                                                                                                SMQ-20
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Abortive Infection Protein
From Lactococcus
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                                      DNA encoding phage
                             resistance
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N/A
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Best Local Similarity Matches 149; Conserv

Conservative

3.9%; Score 39.2; DB 44.9%; Pred. No. 0.14;

DB 1;

Length 4467;

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Mismatches

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS (version SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                         SEQUENCE CHARACTERISTICS:
                                                                                                                 NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Quest 4.1-158
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         FILING DATE: August CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                     TELEFAX:
                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette 5.25 inch, MEDIUM TYPE: 360 Kb storage
                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Michigan
 STRANDEDNESS:
                          LENGTH:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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J. Holler, Peter A. Vandenbergh,
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                                                                                      347-4103
                                                                                                    347-4100
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Abortive Infection Protein
From Lactococcus
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ber 1, 1995
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                                                                                                                                                       Patent No. 5928688
                                                                                                                                                                    Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 149; Conserv
                                                                                                                        GENERAL INFORMATION:
APPLICANT: Sylvai
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             TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
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                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2359 TATTGTCTATATTTTTAGTATCTACTTTTTTTTTTTTCAATGTATTTGTTATAACTGGGA 2300
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ORIGINAL SOURCE:
NUMBER OF SEQUENCES:
                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                     2059 CTTGCTTTTCATTCTCAAAAGTAAACGGAAAT 2028
                                                                                                                                                                                                                                                                                                                                                                               2179 AAGAAAAATATCCGATTTACTCGATTTATCAACAAACGGGAAATTGTCAACTTTCGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: phage abort
LOCATION: N/A
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE: N/A
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                                                                                                                                                                        Application US/08909425P
                                                                                                         Sylvain Moineau, Barbara
J. Holler, Peter A. Vandenbergh,
                                                                          Kondo
                                                                                          Ebenezer R. Vedamuthu,
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                                                           DNA Encoding Phage
                            Abortive Infection From Lactococcus
              lactis, and Method of Use Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39.2; DB 2;
Pred. No. 0.14;
0; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phage
                                              Protein
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ADDRESSEE:

Ian C. McLeod

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NAME/KEY: phage abortive infection; LOCATION: N/A; LOCATION: N/A; IDENTIFICATION METHOD: sequencing OTHER INFORMATION: DNA encoding phage; OTHER INFORMATION: resistance; PUBLICATION INFORMATION: N/A; US-08-909-425A-1
                                                                                                                                              Query Match 3.9%; Score 39.2; DB 2; Length 4.8 Best Local Similarity 44.9%; Pred. No. 0.14; Matches 149; Conservative 0; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (517) 347-4103
TELEX: NO. 5928688e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/565,907
FILING DATE: December 1, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEPAX: (517) 347-4103
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HYPOTHETICAL: NO
""T-SENSE: NO
""VDE: N/A
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MEDIUM TYPE: Diskette 5.25:
MEDIUM TYPE: 360 Kb storage
2299 AAATACATTTTATAGCTCCCTTATTCCCTAAATGTTCTCATTCACACAATAATCTATAA 2240
                                                                      2359 TATTGTCTATATTTTTAGTATCTACTTTTTTTTTTTTCAATGTATTTGTTATAACTGGGA 2300
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LIBRARY: genomic
CLONE: SMQ-20
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PRIOR APPLICATION DATA:
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DESCRIPTION:
                     517 aaatatttggatataatcctttattagatatatagtacaactacacttagtattctgaaa 576
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CELL LINE: N/A
ORGANELLE: N/A
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TYPE: Nucleotide
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CITY: Okemos
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August 11, 1997
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2059 CTTGCTTTTCATTCTCAAAAGTAAACGGAAAT 2028
                                 757 tttactgtttatctggtattctaaagggaaat 788
                                                                                                   ggtttgcttgttcttatggatattgttcataggtaattagtccaatttaattttagctgt 756
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Search completed: September 12, Job time: 14833 sec 2002, 08:12:56

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Result
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                         125.8
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length: 2000000000
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Match Length
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Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tactagcttaagatttccca.....tgtattaaaccagttggaca
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BH022954 GH_MBb000
BG132327 EST465219
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5.2	5.2	5.3	5.3	5.3	5.4	5.4	5.4	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.7	5.7	5.7	5.7	5.8	5.9	6.0	6.0	6.1	6.1	6.2	6.2	6.2
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ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT AV939010 LOCUS BASE COUNT ORIGIN COMMENT FEATURES DEFINITION Query Match source 1 (bases 1 to 678) Sato, K., Saisho, D. and Takeda, K. Barley EST sequencing project in NIG and Okayan Unpublished (2002) Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yatta, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6855 Fax: 81-559-81-6855 AV939010 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum cDNA clone bah20e24 5', mRNA sequence. Hordeum vulgare subsp. spontaneum. Hordeum vulgare subsp. spontaneum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae EST Email: tshini@genes.nig.ac.jp. Location/Qualifiers AV939010.1 GI:18234807 Triticeae; 193 /organism="Hordeum vulgare subsp. spontaneum" /strain="H602" /db_xref="taxon:77009" /clone="bah20e24" /clone="bah20e24" /clone=lib="K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves" /tissue_type="top three leaves" /tissue_type="top three leaves" /dev_stage="adult, heading stage" /dev_stage="adult, heading stage" / dev_stage="adult, heading stage" Hordeum. 12.6%; Score 125.8; DB 9; Okayama Univ Length 678;

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1 (bases 1 to 375)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
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855 California Ave, Palo
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Contact: Walbot V
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Plate: 687002 row: G col
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650 725 8221
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                                                                                                                                                                                                                                                                                                                     Site_2: EcoRI; Library was prepared by Statagene using the Uni-ZAP XR system (Stratagene BN937328-12). Clones were picked by a O-bot after blue/white selection (ampicillin resistance - use 100 micrograms/microliter). Developed from a pool of equal amounts of RNA from developing embryos sampled at 14, 21, 28 and 35 days after pollination of the Illnois High Oil Maize Strain Cycle 90. This closed strain has been selected for high oil concentration for 90 generations and originates from the 1890s era open pollinated variety Burr's White"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="embryo"
/dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. coli SOLR"
/note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
; Site_2: EcoRI; Library was prepared by Statagene using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="Illinois High Oil"
/db_xref="taxon:4577"
/clone_lib="687 - Early embryo from Delaware"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
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taatgcttcatgcacataaaatatttggatataatcctttattagatatatagtacaact
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                                             AGTAGTATAGATATCTCAATTCTTATTGGTTTTTCTTACTGAGGAACATGGCCATTTCTA
                                                                                                           TGCAGAACTATACGCTTTTAGGCCTTTGTACCATGATGCTAGCTGTATCTTCAAGCAACT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 386)
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BP 191 91006 EVRY cedex - FRANCE (
- Web : www.genoscope.cns.fr)
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/strain="Columbia"
/db_xref="taxon:3702"
/clone_lib="TAMU"
/clone="TIH18"
/note="end: T7"
/note="end: T7"
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Pred. No. 3.6e-09;
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segref@genoscope.cns
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BOGTD27TR
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Tel: 301-838-3523
Fax: 301-838-0208
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BH521642
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cdtown@tigr.org
DNA is from a doubled haploid
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1 (bases 1 to 491)
                                                                                                                                                                                                                                                                                         144
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                                                                                                                                                                                                                                                                                       /clone_lib="BOGT"
/note="Vector: pHOS1; Site_1: BstXI; 2
genomic DNA inserted into pHOS1 using
genomic 99 g 159 t
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/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGTD27"
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DEFINITION

L37476 BNAESTCQ

Mustard

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bp mRM Brassica

CDNA linear

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                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 749)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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L37476.1
EST.
                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
High quality sequence stop: 691.
                  Plate: LLAM9701 row: 1 column: 15
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Lim,C.O., Kim,H.Y., Kim,M.G., Lee,S.I., Chung,W.S., Park,S.H.,
                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                             BE905170.1 GI:10398185
                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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                                                                      CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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/strain="pekinensis"
/db_xref="taxon:3711"
/clone="F0956"
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/note="Devel_stage = flower bud "
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100 Jordan Hall, C
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                                                                                                                                                                                                                                 High quality sequence stop:
                                                                                                                                                                                                                                                       Email: rwing@clemson.edu
Class: BAC ends
                                                                                                                                                                                                                                                                                              Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                               Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
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Development of Genomic Resources for Cotton (Gossypium hirsutum
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/tissue_type="epithelioid carcinoma"
/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
137 c 165 g 222 t
                                           /clone="GH_MBb0003022r"
/clone_lib="Gossypium hirsutum L.
/tissue_type="Young leaves"
/lab_host="E. coli"
/note="Vector: pCUGIBAC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation, ordering clones
                                                                                                                            /cultivar="Maxxa"
/db_xref="taxon:3635"
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/db_xref="taxon:9606"
/clone="IMAGE:3901214"
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aatccttgatcgatagagcacatgagcttggtttgcttgttcttatggatattgttcata
                                                                 ggtaccatgttactaatttttttgcaccaagtagccgttttggaactccagaggacttaa 667
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                                                GGTATCATGTTACAAACTTTTTTGCTGTGAGCAGTAGATCTGGAAATCCGGAGGACCTAA 405
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                                                                                                                 87; Conser
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, C. and Tanksley, S.
Generation of ESTs from
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tomato
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Location/Qualifiers
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                                                                                                                                                                                                          /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xho1; Four wk old greenhouse plants were stab inoculated on stem with Agrobacterium tumefaciens C58 (Dr. T.J. Burr Cornell U.). Galls were allowed to develop for another 4 wks, when gall tissue was frozen in liquid nitrogen." 129 c 141 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and sequence analysis see
http://www.genome.clemson.edu/projects/stc/cotton/GH_MBb
a 104 c 106 g 167 t 2 others
                                                                                                                                                                                                                                                                                                                                                         /clone_lib="tomato crown
/tissue_type="crown gall'
                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4081"
/clone="cTOE701"
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Lycopersicon
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                            /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                         /dev_stage="crown galls from full-grown plants (8
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Pred. No. 0.0007
0; Mismatches
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BF272517
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
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Fax: 864 656 4293
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An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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                                                AU061011 Dictyostelium discoideum SL (H.Urus discoideum cDNA clone SLC606, mRNA sequence.
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On Nov 17, 2000 th
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1:
174 c 189 g 263 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="GA__Eb0015C11f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10"
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/strain="AKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:29729"
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Pred. No. 0.0013;
0; Mismatches 3
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                                                                                                                                                                                                                       Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 375)
1 (bases 1 to 375)
Kohara, Y., Motohashi, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A. and Nishigati, A.
                                                                                                                                                                                                                                                                                                                                                                                C68665 375 bp mRNA linear EST 23-
C68665 Yuji Kohara unpublished cDNA Caenorhabditis elegans
clone yk306c3 5', mRNA sequence.
C68665
                                                                                                Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1998)
Contact: Hideko Urushihara
Institute of Biological Sciences
                                                                                                                                                                               Expression map of the C.elegans Unpublished (1996)
Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                   C68665.1 GI:2430021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiani, H. and Tanaka, Y. Developmental cDNA in Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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                                                            ykohara@lab.nig.ac.jp.
Location/Qualifiers
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Dictyostelium discoideum
/dev_stage="slug"
107 c 162 g 208 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="faxon:44689"
/clone="SLC606"
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322 aagataaattcatatgctaattttagggatgaggtgttgccaagaattaaaaggcttgga 381
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 573)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tadasu Shin-i
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                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                        /db_xref="taxon:6239"
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/clone="ykl119c01"
/clone="ib" unpublished oligo-capped cDNA library,
elegans L1 stage"
/elegans L1 stage"
/sex="hermaphrodite"
/tisw_tppe="whole animal"
/dev_stage="L1"
121 c 127 g 155 t 1 others
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/clone_lib="ruji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
10 t
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Caenorhabditis elegans"
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; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 637)
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                            BE704392 "MI-P-E6-acc-d-08-1-UM.sl NMI-P-E6-acc-d-08-1-UM 3', BE704392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="unpublished oligo-capped cDNA library,
elegans L1 stage"
                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="hermaphrodite"
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/dev_stage="L1"
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/strain="N2"
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MI-P-E6 Sus scrofa
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                             429
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                                                                                                                                                                                               Local Sines 102;
                 aagctttgggtattcacacaatccatttttttctgtatacactcttca
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                                                                               taaaaggcttggatacaatgcagtgcagataatggcaatccaggagcattcatactatgc 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cktuggle@iastate.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
Oligo-dT track not found, Not I site shown in beginning of sequence
Oligo-dT track not found, Not I site shown in beginning of sequence
Is likely internal to the message. cDNA Library Preparation: RJ
Woods, JA Green, RS Prather S142 Animal Science Research Center,
Department of Animal Science, University of Missouri-Columbia,
65211 Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Iowa State University
201 Kildee Hall, Ames,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Tuggle CK Molecular Genetics Laboratory, Department
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TAG_SEQ-None found"
99 c 91 g 150 t 1
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Eutheria; Cetartiodactyla; Suina; Suidae;
1 to 487)
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                                                                                                                                                                                              Score 62.4; DB 10;
Pred. No. 0.0052;
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/organism="Aegilops tauschii"
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1 (Pases 1, Li,Z., Mukai,Y., Yamamoto,M., Kosar-Hashemi,B., Abrahams,S. and Morell,M.K.

Rosar-Hashemi,B., Abrahams,S. and Morell,M.K.

Comparison of Starch-Branching Enzyme Genes Reveals Evolutionary Relationships Among Isoforms. Characterization of a Gene for Starch-Branching Enzyme IIa from the Wheat D Genome Donor Aegilops
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EYKRIRAAIDQHEGGLEAFSRGYEKLGFTRSAEGITYREWAPGAHSAALVQDENNWNP
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VLMDIVHSHSSNNTLDGLNGFDGTDTHYFHGGPRGHHWMDSRLFNYGSWEVLRFLLS
NARWHLEEYKFDGFREDGVTSMMYTHHGLQMTFTGNYGSTFFFAPADVDAVVYLMLVND
LIHGLYPDAVSIGEDVSGMPTFCIPVPDGGVGFDYRLHMAVADKWIELLKOSDESWKM
GDIVHTITNRRWLEKCYTYAESHDQALVGDKTTAFWLMOKDMYDFMALDRPSTLRIDR
GIALHKMIRLYTMGLGGEGYLMEMGNEFGHPGNYGETFGNYGDTLFTGNYGNYDKNADSVDK
GIALHKMIRLYTMGLGGEGYLMEMGNEFGHPGNYGDFRCPOTLFTGNYLDRYDKNNSYDK
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Kim,K.-N., Fisher,D.K., Gao,M. and Guiltinan,M.J.
Molecular cloning and characterization of the amy
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                                                                           agagttgttgatcattaaaaatatcatgatttttt------gcagggagatgcagattt 618
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AGCTTTTAAGCAATGAAGGTTTCATTATGAATTCTTTCATGTTGCATCAACAACTCTTAG
                           agatgaaaactgtgcaaaggcggagctggaattgct----tttcaccaaaactattttc 832
                                                          TGAAGTATGTTCTTTTTTACTTTTTTGATTTTGGTTCTGCAAGGTTTCCACAAACATCAT 18590
                                                                                                                                     tggggtatg------tcactggtttgtctttgttgcataacaagtcacagttt
                                                                                                                                                                            TCTTAGGTATCATGGTATGCAAGAGTTTGATCAGGCAATGCAACATCTTGAGCAAAAATA
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                                                                                                                                                                                                                                     TCAATAATTCGTCATTATCGGAATTGTGTTATTTTTACATTGTCAGGGTGATGCAGACTA 18470
                                                                                                                                                                                                                                                                                                 TGCTTTAATCAGCAAGGTGCCATTATAATAGTTCCTTCTTTATTCATATTAGCATGTTCC
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Pred. No. 7.7e-39;
0; Mismatches 333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aacttccactggagcaatagcttttttg 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cggaaacatgaggaagataaggtgatcatcctcaaaagaggagatttggtatttgttttc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rahman,S., Regina,A., Li,Z., Mukai,Y., Yamamoto,M., Kosar-Hashemi,B., Abrahams,S. and Morell,K.
Comparison of Starch-Branching Enzyme Genes Reveals Evolutionary Relationships Among Isoforms. Characterization of a Gene for Starch-Branching Enzyme IIa from the Wheat D Genome Donor Aegilop
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AF338432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rahman, S., Regina, A., Li, Z., Direct Submission
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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DENIMMINADİTMIRDDYĞVWELIFLƏNIADĞSJA I PHĞSRIKI REMDTPĞĞVKDĞISMI
KFŞVQAPGEIPFNGIYYDD PEEEKYVFÖHPQPKRPESLAIYESHIĞMSŞPEPKINSYA
NERDEVLPRIKRLĞYNAVQIMALQEHSYYAŞFÖYHVTNFFAPŞSRFĞIPEDLKĞLIDR
AHELĞILVLMDIVHŞHŞSNNTLDĞLNĞFDĞTDTHYFHĞĞPRĞHHMMDŞRLFNYĞŞWE
VLRFLLSNARWILEEYKFDĞFREDĞVTSMYTHBĞLQMIFTĞNYĞEYEĞFATDVDAVV
YLMLVNDLIHĞLHPDAVŞIĞEDVŞĞMOTFCIPVDĞVĞTVIRFUMAVADKWIELLKQ
SDEŞWKMĞDIVHTITNRRWLEKCVTYAŞFÖYLDYĞALVĞDEYRILDRÇMYDFNALDRP
STPRIDRĞIALKKNIKLYMĞLĞĞEĞYLNFMĞNEĞĞILEĞIYĞYĞFMTŞEHQXVPRA
SDEŞWKMĞDIVHTITNRRWLEKCVTYAŞFÖYLDĞÜNEĞĞILEĞIYÇKYŞKHEEDİXV
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/db_xref="taxon:4565"
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                                                                    {\tt IIFERGDLVFVFNFHWSNSFFDYRVGCSRPGKYKVALDSDDALFGGFSRLDHDVDYFT}
                                                                                                                                                                                                                                                                                                                                                                         /product="starch branching
/protein_id="AAK26822.1"
/db_xref="GI:13447952"
                                                                                                                                                                                                                                                                                                                                                      translation="MATFAVSGATLGVARPPAAAQPEELQIPEDIEEQTAEVNMTGGT/
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McCue, K.F. and Ander
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF286319 2970 bp
Triticum aestivum starch branching
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (11-JUL-2000) United States Department of Agricultural Research Service, 800 Buchanan Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.
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                              WRYSEYRRIRAAIDQHEGGLEAFSRGYEKLGFTRSAEGITYREWAPGAHSAALVGDFN
WWNPHADTMTRODYGVWEIFLENNADGSBAIFHGSRYKIRMTPSGYKDSISAMIKFS
VQAPGELFFROAIYYDDP EEEKYVFQHPOPKRPESLRYYESHLGMSSEPRKINSYANFR
DEVLPRIKRLGYNAVQIMAIQEHSYYASFGYHVTNFFAPSSRFGTPEDLKSLIDRAHE
LGLLVLMDIVHSSNNYLDGLMGFDGTDTHYRHGGPRGHHHMMDSRLFNYGSGFEVLR
FLLSNARWHLEEYKFDGFRFDGVTSMAYTHHGLAMTFTGHVGFBYFGFAFDUDAVVYLR
LVNDLIHGLHPDAVSIGEDVSGMPTFCIFVPDGGVGFDYRLHMAVADKWIELLKQSDE
SWKMGDIVHTLINRRWLEKCVTYAESHDQALVGDKTIAFWLANXDMYDFMALDRPSTP
RIDRGIALHKWIRLFWLGGESYLREWGMFFGHFBWIDFPRGPGTLDFSKYLFGNNU
SYDKGRRFFDLGDADFLRYHGMQEFDQAMQHLEEKYGFMTSEHQYVSRKHEEDKVIIF
                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MATFAVSGATLGVARPAGAGGGLLPRSGSERRGGVDLPSLLLRK
KDSSRAVLSRAASPGKYLVPDGESDDLASPAQPEELQIPEDIEEQTAEVNMTGGTAEK
LESSEPTQGIVETITDGVTKGVKELVVGEKPRVVPKPGDGQKIYEIDPTLKDFRSHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="
149. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="glucosyltransferase; alpha-1,4-glucan;
alpha-1,4-glucan-6-glucosyltransferase"
ERGDLVFVFNFHWSNSFFDYRVGCSRPGKYKVALDSDDALFGGFSRLDHDVDYFTTEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="starch branching enzyme 2"
/protein_id="AAG27623.1"
/db_xref="GI:11037534"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Sbe2"
/EC_number="2.4.1.81"
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/cultivar="Cheyene"
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98.7%;
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Pred. No. 8.3e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology
Institute, National Research Council of Canada, 110 Gymna:
Place, Saskatoon, Saskatchewan S7N 0W9, CANADA
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1 (bases 1 to 2970)
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            /translation="MATFAVSGATLGVARPAGAGGLLPRSGSERRGGVDLPSLLLRK KDSSRAVLSRAASPGKVLVPOGESDDLASPAQPEELQ1 PEDIEGGTAEWNMTGGTAEK KDSSRAVLSRAASPGKVLVPOGESDDLASPAQPEELQ1 PEDIEGGTAEWNMTGGTAEK LESSEPTGGIVETITDGVTKGVFELLVGEKPRVVPKPGDGQKIYEIDDTLKDFRSHLD YRYSEYRRIRAAIDQHEGGLEAFSRGYEKLGFTRSAEGITYREWAPGAHSAALVGDFN WNNPNADTMTRDDYGVWEIFLDNNADGSPAIPHGSRVKIRMDTFSGVKDSISAWIKFS VQAPGEIFFNGIYYDAFEEKKVFQHPOFKREBSLRIYESHIGMSSPERKINSYANFE DEVLPRIKKLGYNAVQIMAIQEHSYYASFGYHVTNFFAPSSRFGTPEDLKSLIDRAHE
                                                                                                                                                                                                                                                                                                /gene=
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a 643 c 774 g 778
                                                                                                                                 /product="1,4-alpha-glucan branching enzyme
/protein_id="CAA72154.1"
/db_xref="G1:1885344"
/db_xref="SPTREMBL:P93691"
                                                                                                                                                                                                                                                                                                                                   /gene="sbe2"
151. .2622
LGLLVLMDIVHSHSSNNTLDGLNGFDGTDTHYFHGGPRGHHWMWDSRLFNYGSWEVLR
                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                           /EC_number="2.4.1.18"
                                                                                                                                                                                                                                         /gene="sbe2"
                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4565"
/clone="pRN33"
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Triticum aestivum"
/cultivar="Fielder"
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hes 148;
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                                                                                                                                                                                                                                                                                           Submitted (08-AUG-1996) University of Hamburg, Institute of General Botany, Centre of Applied Molecular Biology, AMP II, Ohnhorststr. 18, Hamburg 22609, Germany
                                                                                                                                                                                                                                                                                                                                                                      Pooideae; Triticeae; Triticum.

1 (bases 1 to 2853)

Kroeger,C., Loerz,H. and Luetticke,S.
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
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                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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2930. 2935
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                                                                                                                                                                        /tissue_
313. .25
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ERGDLVFVFNFHWSNSFFDYRYGCSRPGKYKVALDSDDALFGGFSRLDHDVDYFTTEH
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LVNDLIHGLHPDAVSIGEDVSGMPTFCIPVPDGGVGLDYRLHAAVADKMIELLKOSDE
SWKWGDIVHTLINRRWLEKCVTYAESHDOALVGDKTLAFWLMDKDMXDEWALDRRSTP
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                                                                                                                                                                                                         /cultivar="T.A. Florida"
/db_xref="taxon:4565"
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                                                                                                                                                                                                                                           /organism="Triticum aestivum"
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                                                                                                                'codon_start=1
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                                                                                                                                                     /EC_number="2.4.1.18"
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/product="1,4-alpha-glucan branching enzyme
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                                                                                                                                                                                                                                                                                                                                               Submitted
Stockholm
                                                                                                                                                                                                                                                                                                                                                                                      Sun,C., Sathish,P., Ahlandsberg,S. and Jansson,C Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sun, C., Sathish, P., Ahlandsberg, S. and J
The two genes encoding starch-branching
differentially expressed in barley
Plant Physiol. 118 (1), 37-49 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare cultivar Bomi starch branching enzyme IIa (sbeIIa) mRNA, nuclear gene encoding plastid protein, complete cds.
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VKIRMTPSGVKDSISAWIKFSVQAPGELPFNGIYYDPPEEKKVFQHPGPKREESLR
IYESHIGMSSEEPKINSYANFKDEVLERIKRIGXYANVOIMAIQEHSYYASFGYHUTUN
FAPSSRFGTPEDLKSLIDRAHELGLLVLMDIVHSHSSNNTLDGLNGFDGTDTHYFHGG
PRGHHMWDSRLENYGSWEVLRRTLLSNARWMLEEYHFOGFFDGOTOSMXTHHGIQMT
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                                                                                                                                                                                                      1. .2554
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               (11-MAY-1998) Stockholm University, Biochemistry, S-10691, Sweden
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                                                                                                                     /EC_number="2.4.1.18"
                                                                                                                                        /gene="sbeIIa"
                                                                                                                                                                               /gene="sbeIIa"
                                                                                                                                                                                                                          /db_xref="taxon:4513"
/chromosome="2"
                                                                                                                                                                                                                                                                                   /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                  ′cultivar="Bomi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triticeae; Hordeum.
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JOURNAL
MEDLINE
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AUTHORS
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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U65948
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Direct Submission
Submitted (02-AUG-1996) Hort./Bi
519 Wartik, University Park, PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gao,M., Fisher,D.K., Kim,K.N., Shannon,J.C. and Guiltinan,M.J. Independent genetic control of maize starch-branching enzymes and IIb. Isolation and characterization of a Sbe2a cDNA Plant Physiol. 114 (1), 69-78 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays
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                                                                     /gene="Sbe2a"
/EC_number="2.4.1.18"
/function="formation of alpha-1-6 glucosidic linkage starch biosynthesis"
/note="starch branching enzyme isozyme SBEIIa"
                                                                                                                                                                                              /gene=
<1. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      starch branching enzyme IIa (Sbe2a) mRNA, partial cds
                                                                                                                                                                                                                                                                                                                                   ...versity Park, PA 16802, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGHPEWIDFPRGPQTLPTGKYLPGNNNSYDKCRRRFDLGDADFLRYRGMQEFDQAMQH
LEEKYGFMTSEHQYVSRKHEEDKVIIFERGDLVFVFNFHWSNSKKDYRVGCSKPGKYK
VALDSDDALFGGFSRLDHDVDYFTTEHPHDNRPRSFSVYTPSRTAVVYALTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YFHGGPRGHHWMWDSRLFNYGSWEVLRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHH
GLQMTFTGNYGEYFGFATDVDAVVYLMLVNDLIHGLYPDAVSIGEDVSGMPTFCIPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHGSRVKIRMDTPSGVKDSISAWIKFSVQAPGEIPFNGIYYDPPEEEKYVFQHPQPKR
PESLRIYESHIGMSSPEPKINSYANFRDEVLPRIKRLGYNAVQIMAIQEHSYYASFGY
HVTNFFAPSSRFGTPEDLKSLIDRAHELGLLVLMDIVHSHSSNNTLDGLNGFDGTDTH
                                                                                                                                                                                                                                                                                 /strain="B73"
/db_xref="taxon:4577"
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/product="starch branching enzyme IIa"
/protein_id="AAB67316.1"
/db_xref="GI:2340108"
                                                                                                                                                                                                                                                             /note="inbred"
                                                                                                                                                                                                                                                                                                                            /organism="Zea mays"
                                                              /codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:2340107
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96.0%;
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Pred. No. 2.1e-18;
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ORIGIN

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SOURCE

KEYWORDS VERSION ACCESSION

FEATURES

gene CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 aggatatgtatgatttcatggctctggatagg-cttcaactcttcgcattgatcgtggca 101
                                                                                                                             MITSUI GYOSAI SHOKUNITSU BIO KENKYUSHO:KK, MITSUI PETROCHEM IND LTD
OS OTYZA SATIVA (rice)
PN JP 1998004970-A/2
PD 13-JAN-1998
PF 24-JUN-1998 JP 1996162983
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JP 1998004970-A/2.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryza.
333
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NEW RICE GENE FOR STARCH-BRANCHING ENZYME
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VDTQPEELQIPEABLIVEKTSSSFTQTTSAVABASGVVBAEERFELSEVIGVGGTGGT
KIDGAGIKAKAPLVEEKFRVLPPFGDGQRIYEIDPMLEGFRGHLDYRYSEYKRLRAI
DQHEGGLDAFSRGYEKLGFTRSAEGITYREWAPGAYSAALVGDFNNWNPNADAMARNE
YGVWEIFLPNNADGSPAIPHGSRVKIRMDTPSGVKDSIPAWIKFSVQAPGEIPYNGIY
YDPPEEKYVFKHPQPKRPKSLRIYESHYGMSSPEPKINTYANFFDEVLPRIKKLGYN
AVQIMALQEHSYYASFGYHYTNFFAPSSRFGTPEDLKSLIDKAHELGLLVLMDIYHSH
SSNNTLDGLNGFDGTDTHYFHGGPRGHHMMNDSRLFNYGSWEYLMFLKSLAKWWILEEY
KFDGFRFDGTTSMMYTHHGLQVTFTGNYGEYFGFATDVDAVYLMLVNDLIRGLYPEA
VSIGERPGTSMMYTHHGLQVTFTGNYGEYFGFATDVANVYLMLVNDLIRGLYPEA
VSIGERPGTSMYTHHGLQVTFTGNYGEYFGATDVANVYLMLVNDLIRGLYPEA
VSIGERPGTSMYTHHGLQVTFTGNYGEYFGATDVANVYLMLVNDLIRGLYPEA
VSIGERPGTSMYTHHGLQVTFTGNYGEYFGATDVANVYLMLVNDLIRGLYPEA
VSIGERPGTSCHOOLOGGYGFDYRLHMAVPDKWIELLKQSDEYWEMGDIVHTTITN
RRWLEKCVTYCESHDQALVGDKTIAFWLMDKDMYDFMALDRESTPRIDRGIAHKMIR
RRWLEKCVTYCESHDQALVGDKTIAFWLMDKDMYDFMALDRESTPRIDRGIAHKMIR
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ADYLRYRGMQEFDQAMQHLEGKYEFMTSDHSYVSRKHEEDKVIIFERGDLVFVFNFHW
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92.7%;
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                           /tissue_type='Immature Seed'
/clone='prB41'
                                                                                                          /clone_lib='Rise Immature Seed
A library'
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Pred. No. 1.1e-16;
0; Mismatches 10
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Best Local :
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                                                                                                                                                                          AL PATENT: JP 198004970-A 1 13-AN-1988;

MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK, MITSUI PETROCHEM IND LTD OS OTYZA SATIVA (Tice)
PN JP 1998004970-A/1
PD 13-JAN-1998
PF 24-JUN-1996 JP 1996162983
PI BABA TADASHI, KAWASAKI TSUTOMU, ICHIKAWA NORIO PC C12N15/09, A01H5/00,C07H21/04,C12N5/10,C12N9/10,(C12N9/10,(C12N15/09, PC C12R1:91), (C12N9/10,C12R1:19);
PC (C12N5/10,C12R1:91),(C12N9/10,C12R1:19);
CC strandedness: Double;
FC (topology: Linear;
FH Key Location/Qualifiers
FH Key 1. .3015
FT source 1. .3015
FT source 1. .3015
COLOR_11b-'Rice Immature Seed Lambda gtII FT CDNA library'
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E14723
E14723.1 GI:570940
JP 1998004970-A/1.
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1 (bases 1 to 3015)
Baba, T., Kawasaki, T. and Ichikawa, N.
NEW RICE GENE FOR STARCH-BRANCHING ENZYME
Patent: JP 1998004970-A 1 13-JAN-1998;
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Oryza sativa
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Location/Qualifiers
1...2364
              /organism="Oryza sativa"
/db_xref="taxon:4530"
606 c 819 g 794
                                                            Location/Qualifiers
1. .3015
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454 c 600 g
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                                                                                                                                                                    cDNA library'
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                                                                                                                       /tissue_type='Immature seed'
/clone='pRB41'
129. .2654
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                                                                                                       /product='branching
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-FEB-1999) Kouichi Mizuno, University of Tsukuba, Institute of Agricultural and Forest Engineering; 1-1-1 Tennoudal, Tsukuba, Ibaraki 305-8572, Japan (E-mail:koumno@sakura.cc.tsukuba.ac.jp, Tel:81-298-53-4656, Fax:81-298-55-2203)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 3015)
Mizuno, K. and Baba, T.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa tissue_lib:developing seeds cDNA to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecular cloning and expression analysis of a novel member of starch branching enzyme isoform in developing rice seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mizuno, K.,
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STSRGVVSCAGARGKVLYVGGGSDDLLSSAERDVETQEQEESGI PDDNKVKPFEEEE
EIPAVAEAS IKTVAEENLESSEVIGDIEENVTEGVIKDADEPTVEDKTRVIPPOGGG
KIYQIDEMLEGFRNHLDYRYSEYKRMRAAIDQHEGGLEAGYEKLGFTRSAEGITY
REWAPGAQSAALVGDENNWAPNADTMTENEYGVWEISLUNNADGSPAIPHGSRVKIRM
DIPSGVKDSIPAWIKFAVQAPGEIPYNGIYYDPEEEKVYVGHPPQFKRRNSLRYYESH
IGMSSPERINTYANFRDEVLFRIKKLGYNAVQIMAIQHSYYASFGYHVTNFFAPSS
REGTPEDLKSLIDAHHELGLLVLMDIVHSHASNNTLDGLNGFDGTDTHYFHGGGRGHH
WMWDSRLFNYGSWEVLRYLLSNARWWLEEYKGDFFFDGVTSMMYTHHGLQVAFTGNY
GEYFGFAIDVDAVYLMLVNDLLHGLYPEAVAIGEDVSMPTFCIPVODGGVGFDYRL
HMAVDDKWIEILKQSDEYWKNDDIVHTNRRWSEKCYTYAESHDQALVGDKTIAFWL
HMAVDDKWIEILKQSDEYWKNDDIVHTNRRWSEKCYTYAESHDQALVGDKTIAFWL
                                                                                                                                                                                                                                                                                                                                                                                   /product="starch branching
/protein_id="BAA82828.1"
/db_xref="GI:5689138"
                                               GGFSRLDHDAEYFTADWPHDNRPCSFSVYTPSRTAVVYALTED'
                                                                                       MDKDMYDFMALDRPSTPRIDRGIALHKMIRLVTMGLGGEGYLNFMGNEFGHPEWIDFP
RGPQSLPNGSVLPGNNYSFDKCRRRFDLGDADYLRYHGMQEFDQAMQHLEEKYGFMTS
                                                                      <u>EHQYISRKHEEDKVIIFERGDLVFVFNFHWSNSYFDYRVGCLKPGKYKIVLDSDDGLF</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="RBE4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="RBE4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
/db_xref="taxon:4530"
/tissue_lib="developing seeds"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tachibana, M., Kobayashi, E., Kawasaki, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.9%;
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Pred. No. 5.5e-16;
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MZEGLUCTRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.

1 (bases 1 to 2725)

Keeling, P. and Guan, H.
Starch encapsulation
Patent: US 6107060-A 14 22-AUG-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
AR106495
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 2725)
Fisher, D.K., Boyer, C.D. and Hannah, L.C.
Starch branching enzyme II from maize endosperm
                                                                                                                                      Corn s
                                                                                  1,4-alpha-glucan branching enzyme; an
glucanotransferase; starch branching
Zea mays cDNA to mRNA.
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                                                                            Zea mays
                                                                                                                         L08065.1 GI:168482
                                                                                                                                                              MZEGLUCTRN
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534 c 715 g
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Pred. No. 3.
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3.1e-14;
hes 17;
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ng enzyme II.
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 aggatatgtatgatttcatggctctggatag-gcttcaactcttcgcattgatcgtggca 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAGCATTACATAAGATGATTAGGACTTATCACAATGGGTTTAGGAGGAGAGGGCTATCTTA
                                                                                                          Oryza sativa.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 419)
                                                                                                                                                                                                                                                                      Oryza sativa granule-bound starch AF451191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant Physiol. 102, 1045-1046 (1993) 94105320
                                  Unpublished
                                                        Expression and regulation metabolism in rice
                                                                                                                                                                                                                                                   AF451191.1
                                                                                                                                                                                                                                                                                                            AF451191
                                                                                              Lee, D.-S. and Hur, Y
(bases 1 to 419)
e,D.-S. and Hur,Y
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YYGSFGYHYTNFFAPSSRFGTPEDLKSLIDRAHELGLLYLIDVYHSHASSNTLDGLNG
FDGTDTHYFHSGPRGHHWMDDSRLFHYGNWEYLRFLLSNARWHLEEYKFDGFRFDGVT
SMMYTHHGLQVTFTGNFNEYFGFATDVDAVVYLMLVNDLIHGLYPEAVTIGEDVSGMP
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AQALKRVRVVPPPSDGQKIFQIDPMLQGYKYHLEYRSILYRIBGIDEHEGGLEAFS
RSYEKEGENASABGITYFEMAPGAFSAALVGDVNNWDDNADRWSKNEFCVMEIFLJAW
ADGTSPIPHGSRVKVRMDTPSGIKDSIPAWIKYSVQAPGEIPYDGIYYDPPEEVKYVF
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FDQAMQHLEQKYEFMTSDHQYISRKHEEDKVIVFEKGDLVFVFNFHCNNSYFDYRIGC
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ESHDQALVGDKTIAFWLMDKDMYDFMALDRPSTPTIDRGIALHKMIRLITMGLGGEGY
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/protein_id="AAA18571.1"
/db_xref="GI:168483"
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/dev_stage="29 days post pollenation"
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/db_xref="taxon:4577"
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Pred. No. 3.1e-14;
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Submitted (23-NOV-2001) Biology, Chungnam National University, 220
Kungdong, Yuseong-ku, Taejon 365-764, Korea
Location/Qualifiers
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/db_xref="taxon:4530"
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AAX34650
Starch branching enzyme II (SBE II) gene sequence
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                           05-JUL-1999
                                                     AAX34650;
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                          (first entry)
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Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSS; starch branching enzyme; starch soluble synthase; debranching enzyme; endosperm; wheat; barley; granule-bound synthase; glutenin; starch; grain softness protein I; bacterial isoamylase; glycogen synthase; Triticum tauschii. wSBE I-D4 gene; ss.

(CSIR) (GOOD-) (LIMA-) 20-MAR-1998; 12-SEP-1997; 11-SEP-1998; 25-MAR-1999. WO9914314-A1 COMMONWEALTH SCI & IND RES ORG.
GOODMAN FIELDER LID.
GRP LIMAGRAIN PACIFIC PTY LTD.
UNIV AUSTRALIAN NAT. 98AU-0002509. 97AU-0009108. 98WO-AU00743

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                                                The present sequence encodes a wheat starch branching enzyme of Aegilops tauschii, designated F2. A. tauschii is likely to be the ancestral D genome donor of wheat. Probes isolated from the presen sequence were used to identify type II starch branching enzymes (S in wheat, especially BEIIb. The BEIIb nucleic acids may be used to genetically transform cereal plants such as wheat or barley and fo altering their nutritional content by modulating the starch biosynthetic pathway to vary levels of amylopectin and/or amylose produced in the plant.
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Pred. No. 1.3e-47;
0; Mismatches 333;
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/*tag= ae /number= 10 8465.8584 /*tag= af /number= 11 8585.1260 /*tag= ag /number= 11 12605.12734 /*tag= a /number= 12 12735.12820

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                                                                                                                                                                                                                                                                                                                                                           1907
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                                           Wheat; starch | gelatinisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding wheat starch branching enzyme IIb, altering the amylose and amylopectin content of cereal pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wheat; starch branch
starch biosynthetic
  Triticum
                                                                                                                                                      25-JUL-2000
                                                                                                                                                                                                                                             AAZ99942 standard;
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(GOOD-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148;
                                           starch branching enzyme II; SBEII; SBEII-2; starch; SBEII-1;
nisation onset; transgenic plant; foodstuff; bakery product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMONWEALTH SCI & IND RES OR
GOODMAN FIELDER LTD.
GRP LIMAGRAIN PACIFIC PTY LTD
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Pred. No. 1.9e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated starch gelatinization onset and/or peak temperature -
                                                  Triticum aestivum
                                                                          gelatinisation
                                                                                                                Nucleotide
                                                                                                                                                                                          AAZ99947 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 979
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                                                                      starch branching enzyme in sation onset; transgenic
                                                                                                             sequence of starch branching enzyme II clone B11
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                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 foodstuff, particularly bakery products.
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                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                         13.3%;
                                                                      enzyme II; SBEII; SBEII-1;
reneggenic plant; foodstuff;
                                                                                                                                                                                            977
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                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                        starch; SBEII-2;
bakery product;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 979;
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The present sequence represents a clone of wheat starch branching enzyme II (SBEII), which is part of a novel subclass of known SBEII genes, designated SBEII-1. The specification also describes subclass SBEII-2 sequences. The SBEII-1 genes are thought to have similar functional properties to the maize SBEIID gene. Starch branching enzymes catalyse the formation of the alpha-1,6 linkages, creating branch points in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed by reattachment of the released alpha-1,4-glucan chain to the same or another glucosyl chain. SBEII polypeptides can be used to alter the characteristics of a plant, in particular to alter starch so that it has an elevated gelatinisation onset and/or peak temperature. Starch obtained from transgenic plants is useful in the preparation or
Triticum aestivum
                              Wheat; starch branching enzyme II; SBEII; SBEII-1;
gelatinisation onset; transgenic plant; foodstuff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gelatinization onset and/or peak temperature
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                                                                            sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 5.7e-24
0; Mismatches
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RESULT PAAVO 5639 ID AAVO 5639 ID AAVO 5639 ID AAVO XX AAVO DT 01-M Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Rice XX Ri
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mat_peptide
                                               sig_peptide
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                                                                                                                                                                                                                                  Rice;
                                                                                                                                                                                                                                                                               Rice type IV
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Location/Qualifiers
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/*tag- a
129.287
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288.2651
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97.3%;
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Pred. No. 5.7e-24;
                                                                                                                                                                                                                                                                               enzyme cDNA
                                                                                                                                                                                                                            enzyme; amylopectin synthesis;
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RESULT AAZ9962 ID AAZ9 XX AAZ9 XX CONS CONS XX Whea KW Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX Gela XX
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes the rice type IV starch branenzyme, which has the ability to synthesise amylopectin. quality of starch is improved by the use of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2128
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                                                                   (PLAN-) PLANT BREEDING INT CAMBRIDGE
                                                                                                                                                                   09-SEP-1999;
                                                                                                                                                                                                                                                                  WO200015810-A1.
                                                                                                                                                                                                                                                                                                                  Triticum
                                                                                                                                                                                                                                                                                                                                                                 gelatinisation
                                                                                                                                                                                                                                                                                                                                                                                        Wheat;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ99962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ99962 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2008 aggatatgtatgattttatggctctagacagaccttcaacacctcgcattgatcgtggga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Pages 5-8; 13pp; Japanese.
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                                                                                                                     10-SEP-1998;
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(MITK ) MITSUI TOATSU CHEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 acttcatgggaaatgagtttgggcatcctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 aggatatgtatgatttcatggctctggatag-gcttcaactcttcgcattgatcgtggca
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                                                                                                                                                                                                                                                                                                                                                            starch branching enzyme II; SBEII; SBEII-1;
nisation onset; transgenic plant; foodstuff;
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                                                                                                                     98EP-0307337.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  of starch branching enzyme
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91.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 118.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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bakery p
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                                                                                                                                                                                                                                                                                                                                                            product;
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Goldsbrough

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RESULT 10
AAT69737
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Best Local S
Matches 133
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Transgenic corn in which grain derived starch fine structure is controlled - specifically branch chain distribution of amylopec useful in preparation of thickened foodstuff
                                                                                                                                                                                                                                                                                                 Starch branching enzyme IIb; SI amylopectin; transgenic plant;
                                                                                       Broglie KE,
                                                                                                                                                                                                                                                                                                                                              Corn starch
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT69737 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gelatinization onset and/or peak temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding wheat starch branching enzyme II isoforms, useful in altering the characteristics of a plant, especially elevated stargelatinization onset and/or peak temperature -
                                                          WPI; 1997-341694/31
                                                                                                                                                   20-DEC-1995;
                                                                                                                                                                                 12-DEC-1996;
                                                                                                                                                                                                              26-JUN-1997.
                                                                                                                                                                                                                                          WO9722703-A2
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                                                                                                                      (DUPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ttatgggaaatgagtttgggcatcctg 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cattacataaaatgatcaggcttgtcaccatgggtttaggtggtggaggctatcttaact
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DU
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                                                                                                                        PONT
                                                                                                                                                                                                                                                                                                                                              branching enzyme
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                                                                                         Hubbard
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                                                                                                                                                   95US-0009113
                                                                                                                                                                                 96WO-US19678
                                                                                                                      DE NEMOURS
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                                                                                         NL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.4%;
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                                                                                         Klein
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                                                                                                                      င္ပ
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                                                                                                                                                                                                                                                                                                                                              IIb gene fragment in pBE96.
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Pred. No. 8.
                                                                                                                                                                                                                                                                                                   pBE96; ss
                                                                                         IM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2e-20;
                                                                                                                                                                                                                                                                                                                maize; antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВB
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               of amylopectin
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RESULT 11
AAT69736/c
ID AAT697
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Best Local
                                                                             Transgenic corn in which grain derived starch fine structure controlled - specifically branch chain distribution of amylog useful in preparation of thickened foodstuff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragment of corn starch branching enzyme IIb (SBEIIb) cDNA (see also ART69729), starting at the initiating ARG codon of the coding region and terminating 312 bp 5' of the translation termination codon. It was obtd. by site-specific mutagenesis of the SBEIIb gene in plasmid pBE240 to generate an NcoI site at the ARG start site, and EcoRI digestion of the mutagenised plasmid. The 2.09 kb fragment was inserted, in sense orientation, between the zein promoter and 3' regions in vector pML103 to produce pBE96. Co-suppression and antisense techniques can be used to inhibit SBEIIb in transgenic plants and thereby alter starch properties.
                entire
                           A 2.16
                                                                                                                                                            Broglie KE,
                                                                                                                                                                                                                                                                                                                                               Starch branching enzyme IIb; SBEIIb; corn; amylopectin; transgenic plant; pBE45; ss.
                                                                                                                                                                                                                                                                                                                                                                                     Corn starch
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                                                     Example 3;
                                                                                                                                    WPI; 1997-341694/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT69736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT69736 standard;
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                                                                                                                                                                                      (DUPO)
                                                                                                                                                                                                                                          12-DEC-1996;
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  of 5 &
                                                                                                                                                                                      Ы
cDNA insert (AAT69736) in plasmid pBE45 comprises the untranslated region as well as 2.08 kb of the coding corn starch branching enzyme IIb (SBEIIb) cDNA (see
                                                     Page 55-56;
                                                                                                                                                                                      PONT DE
                                                                                                                                                                                                                                                                                                                                                                                     branching enzyme IIb gene fragment in
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         The specification describes a method for the production of non-glycogen-like polysaccharides in a host. The method comprises transforming a host, suitable for fermentation, with genes encoding starch or glycogen synthesis enzymes, and fermenting the transformants. The specification also describes hosts transformed with a gene active in glycogen synthesis and at least one non-starch branching gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               also AAT69729). It was generated by EcoRI digestion of plasmid pBE240 and was inserted into vector pML103 in antisense orienta with respect to a maize 27 kDa zein promoter and a 10 kDa zein 3' sequence. Transgenic corn plants expressing the near full-length SBEIID antisense transcript demonstrated a unique starch
                                                                                                                         Producing non-glycogen-like polysaccharides in bacteria, fungi or plants - transformed with genes for enzymes involved in starch or glycogen synthesis allows fermentative production of starches with
                                                                                                                                                                                                                                                                                                                                                     Zea
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A cDNA insert (AAT69729) in plasmid clone pBE240 comprises a EcoRI-XhoI fragment isolated from a corn cDNA library. It is an open reading frame encoding starch branching enzyme IIb (AAW19212). The insert was used as a starting point in the of DNA constructs (see also AAT69730, AAT69736-37) designed achieve suppression of SBEIIb expression in transgenic corn and thereby to produce novel starches that have properties beneficial in food and industrial applications.
                                                                                                                                                                                                                                                     Transgenic corn in which grain derived starch fine structure is controlled - specifically branch chain distribution of amylopectin, useful in preparation of thickened foodstuff
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P-PSDB; AAW19212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used to produce plant-like starches by fermentation in plants. These starches are useful for all food and ications of starch. The present sequence is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0009113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US19678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insert
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(SBEIIb)
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 132
                    comprising a starch-encapsulating region (SER) fused to a payload protein. The hybrid polypeptide can be used to make modified starches comprising the payload protein, selected from,
                                                      The sequence is that of the starch branching It can be used in the production of a hybrid
                                                                                                              Hybrid polypeptide comprising starch-encapsulating region and protein - useful for, e.g. producing protein(s) resistant to degradation by stomach acids
                                                                                                                                                                                                Guan
                                                                                                                                                                                                                                                                  30-SEP-1997;
                                                                                                                                                                                                                                                                                                                                              mat_peptide
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                                                                                           Example
                                                                                                                                                               P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                     sig_peptide
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  immunoglobulins,
                                                                                                                                                                                                                     (EXSE-)
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           g. hormones, growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 132; Conserv
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ch branching enzyme II;
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DB; AAW56489.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acttcatgggaaatgagtttgggcatcctg 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tagcattacataagatgattagacttatcacaatgggtttaggaggagagggctatctta
                                                                                         2; Page 44; 156pp; English.
                                                                                                                                                                                                                      EXSEED
                                                                                                                                                                                             Keeling P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2665 BP;
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265..2487
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91..264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                branching
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  etc. The modified starch can also be used
                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       700 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry 
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             factors, antibodies, enzymes,
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                                                                                                                                                                                                                                                                                                                                                                                  starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                 branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΙΙ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vector;
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                                                                                                                                                                                                                                                                                                                                                                                  enzyme
                                                    enzyme II gene.
polypeptide
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Best Local S
Matches 132
              The rice starch branching enzyme is encoded AAQ73750. The starch content of rice grains increasing the expression of branching enzym
                                                                                                                                                                                                                                                                                                                                                                                                   1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to provide grain feeds enriched in amino acids. By encapsulating the payload protein in starch, it is more resistant to degradation by stomach acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                 1907
                                               Claim
                                                            New gene of branching enzyme of increasing starch yield of rice
                                                                                                                                                                          JP06261767-A
                                                                                                                                                                                                 3'UTR
                                                                                                                                                                                                                                                        5'UTR
                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                              Oryza
                                                                                                                                                                                                                                                                                             Starch branching
                                                                                                                                                                                                                                                                                                            Rice starch branching
                                                                                                                                                                                                                                                                                                                            05-JUL-1995
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                                                                                      P-PSDB;
                                                                                                            (MITS-) MITSUI GYOSAI
                                                                                                                           29-OCT-1992;
                                                                                                                                           22-OCT-1993;
                                                                                                                                                           20-SEP-1994
                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                       transit_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                  162
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                                                                                              1994-337418/42.
                                               ۲,
                                                                                                                                                                                                                                                                               sativa.
                                                                                      AAR60811.
                                              Page 9-12; 13pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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128..322
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2603..2919
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323..2606
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88.0%;
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                                                                                                                                                                                                                                                                                              rice;
                                              Japanese.
                                                                                                                                                                                                        branching_enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 110.8;
Pred. No. 8.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                              starch
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No. 8.3e-19;
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                                                                                                             KENKYUSHO
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               enzyme in
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                       by the cDNA sequence can be increased by
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                                                                      useful
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               plants.
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Sequence 2919 BP;

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Query Match
Query Match
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Query Matches 129; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
Matches 129; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
Qy 43 aggatatgtatgatttcatggctctggatag-gcttcaactcttcgcattgatcgtggca 101
Qb 1962 aggatatgtatgattttatggctctggacagaccggcaacacctaggctatctta 161
Qy 102 tagcattacataaaatgatcaggcttgtcaccatgggtttaggtgtgaaggctatctta 161
Qb 2022 tagcattgcataaaatgattagacttatcacaatggggttaggaggagaggctatctta 2081
Qy 162 acttcatgggaaatgatttaggcttctggacatgggttaggaggagaggctatctta 2081
Qy 162 acttcatgggaaatgagtttgggcatcctg 191
Qy 162 acttcatgggaaatgagtttgggcatcctg 191
Db 2082 actttatgggaaatgagtttgggcatcctg 2111
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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2: /cgn2_6/ptodata/1,

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ALIGNMENTS

Title:

Run on:

US-08-941-445A-14 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/8/941,445A FILING DATE: 30-SEP-1997 CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/026,855 FILING DATE: 30-SEP-1996 ATTORNEY/AGENT INFORMATION: NAME: Winner, Ellen P REGISTRATION NUMBER: 28,547 BRETEPENCE/DOCKET NUMBER: 89-97 Sequence 14, Application US/08941445A Patent No. 6107060 TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 2725 base pairs GENERAL INFORMATION: REFERENCE/DOCKET NUMBER: 89 TELECOMMUNICATION INFORMATION: APPLICANT: Keeling, Peter APPLICANT: Guan, Hanping TITLE OF INVENTION: Starch Encapsulation NUMBER OF SEQUENCES: 37 TOPOLOGY: not relamOLECULE TYPE: mRNA HYPOTHETICAL: NO CORRESPONDENCE ADDRESS: ORGANISM: STRANDEDNESS: TYPE: nucleic acid TELEPHONE: (303) 499-8080 ZIP: 80303 COUNTRY: STREET: 5370 | CITY: Boulder ADDRESSEE: င္ပ SOURCE: E: Greenlee, Winner and Sullivan, 5370 Manhattan Circle SS: single not relevant sig_peptide 91..264 Zea mays P.C.

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TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER FILING DATE: 1998-19-27/SE96/01558
EEARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1995-11-29
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LARSSON, Hakan APPLICANT: RASK, Lars
                                                                                   FEATURE: misc_feature NAME/KEY: misc_feature LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are OTHER INFORMATION: n wherein n = A, C, G of T.
                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                  NAME/KEY: misc_feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amin
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LOCATION: (333)..(2825)
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LOCATION: (189)..(332)
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TYPE: DNA
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                  Xaa wherein
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; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino
US-09-087-277-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/087,277B CURRENT FILING DATE: 1998-05-29 EARLIER APPLICATION NUMBER: PCT/SE96/01558 EARLIER FILING DATE: 1996-11-28 EARLIER APPLICATION NUMBER: SE 9504272-7 EARLIER FILING DATE: 1995-11-29
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF LIVENTION: STARCH BRANCHING ENZYME II
FILE REFERENCE: 003300-486
                                                                                                                                                                                                                           SOFTWARE: PatentIn
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1996-04-19
                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: SE 9601506-0
   NAME/KEY:
                                 LOCATION: FEATURE:
                                                                                                OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                             TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1896)..(1898)
OTHER INFORMATION: Amino
OTHER INFORMATION: or Phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: (1428)..(1430) OTHER INFORMATION: Amino
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NAME/KEY: misc_feature
LOCATION: (1404)..(1406)
OTHER INFORMATION: Amino
                                                                                 FEATURE:
                                                               NAME/KEY:
                                                                                                                                                                                            LENGTH: 1393
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misc_feature
(424)..(1150)
                                              CDS
(2)..(1393)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KHOSNOODI, Jamshid
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LARSSON,
                                                                                                                                                                                                                              Ver.
                                                                                                (potato)
                                                                                                             Description (branching )
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Pred. No. 3.5e-17;
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                                                                                                               enzyme II) i
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                                                                                                                            of
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                                                                                                                 from Solanum tuberosum
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                                                                                                                                fragment
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; NAME/KEY: misc_feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa =
US-09-087-277-3
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US-08-716-449-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08716449 Patent No. 6103893
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 124;
TELEFAX: (410) INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (890)..(892)
OTHER INFORMATION: Amino acid 297 is Xaa
OTHER INFORMATION: or Phe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: (422)..(424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Nucleotides 424, OTHER INFORMATION: C, G or T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00634
FILING DATE: 22.03.95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1166 gatcgtgggatagcattgcacaagatgattaggcttgtaactatgggattaggaggagaa 1225
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                                                                                           REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 ggctatcttaacttcatgggaaatgagtttgggcatcctg 191
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: FILED
                                                                                                                                                                                                                                                                                                                                               COMPUTER: COMPAQ
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: IMB 1.44 MB High Density Diskette COMPUTER: COMPAQ Deskpro 590 (IBM PC compatible OPERATING SYSTEM: WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
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                                                                         TELEPHONE:
                                                                                                                                   NAME: Anita E.Nador REGISTRATION NUMBER:
                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Canada M5K 1H6
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Box 194, 24th Floor, Toronto-Dominion Bank Tower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Starch and Chemical Investment
Holding Corporation
VENTION: Method for Producing Altered Starch
                                                                                                                                                                                                                                                                                                                             Word 7.0 for Windows
                                                     (416) 368-2400
116) 363-7246
                                                                                                                                                                                                                                                                     UMBER: US/08/716,449
FILED CONCURRENTLY H
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77.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from Potato
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Pred. No. 7
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7.1e-17;
                                                                                                                                                                                                                                                                                                                                                                 compatible)
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                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/08941445A Patent No. 6107060
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Best Local 9
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                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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CIONE: 1.2.1 and E2
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1781
                                                                                                                                                                                                                                                      APPLICANT: Keeling, Peter
APPLICANT: Guan, Hamping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
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ANTI-SENSE: NO
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD: lone ORF with homology to othe IDENTIFICATION METHOD: branching enzymes OTHER INFORMATION: complements KV832 E. coli glycogen OTHER INFORMATION: branching enzyme mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: starch branching enzyme LOCATION: 44-2788
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STRAIN: cv desiree
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     APPLICATION NUMBER: FILING DATE: 30-SE
                                                                                                                                      COUNTRY: UI
                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGGCCTTGGGAGGAGAGGGGTACCTCAATTTCATGGGTAACGAGTTTGGCCATCCTG 1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGCTTCTCCTGTTGTTGATCGAGGAATTGCGCTTCACAAGATGATCCATTTTTTCACA 1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Similarity
| 82; Conserv
                                                                                                                                                                                         Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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                                                                                                                                                                                                       5370 Manhattan
                                                                                                                                                       SD
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                                                                                                                                                                                                       Greenlee, Winner and
70 Manhattan Circle
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O
UMBER: US/08/941,445A
30-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lone ORF with homology to other starch
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US-08-104-158-1
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                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Approximately No. 621504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Willmi
APPLICANT: Sonnew
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                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1692 AGCCTGCTTCACCTACAATTGATCGAGGGATTGCACTCCAAAAGATGATTCACTTCATCA 1751
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                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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LOCATION:
                                                                          COUNTRY: U.S.A. ZIP: 10036-8403
                                                                                                      CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 89-97
                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                      Application US/08104158
                                                                                         New York
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                                                                                                                                  E: Ostrolenk, Faber, Gerb & 1180 Avenue of the Americas
                                                                                                                                                                                                                                                   Jacobsen, Evert
                                                                                                                                                                                                                                                                 Mueller-Roeber, Bernd
Visser, Richard Gerardus Francisus
                                                                                                                                                                                                                                                                                               Sonnewald, Uwe
Kossmann, Jens
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ilarity 68.3%;
Conservative
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191..2467
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not relevant
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Th NO: 16:
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                                                                                                                                                                                                       PLASMIDS CONTAINING DNA-SEQUENCES THAT CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
                                                                                                                                                                                            AND PLANTS CONTAINING THESE PLASMIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 60/026,855
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Pred. No. 2.6e-07;
0; Mismatches 38
                                                                                                                                               Gerb & Soffen
    Version
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      #1.25
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RESULT 7
US-08-844-188-39/c
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                                                                                                                                                                                                                            Sequence 39, Application US/08844188 Patent No. 6127180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                           GENERAL INFORMATION:
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TELEX: 236925
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NC ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P
FILING DATE: 13-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                  CORRESPONDENCE ADDRESS:
                                                    APPLICANT: Schwab, George E.
TITLE OF INVENTION: Pesticidal Toxins
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                         1661 AATGGCCTTGGGAGGAGGGGTACCTCAATTTCATGGGTAACGAGTTTGGCCATCCTG 1719
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APPLICATION NUMBER: EP PCT/EP92/00302
FILING DATE: 11-FEB-1992
                                                                                                              APPLICANT:
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LOCATION: 2..1699
COTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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LIBRARY: cDNA of total tuber mRNA in pUC 19 (Hinc
                                                                                                                                                                                                                                                                                                                                                              133 catgggtttaggtgatggctatcttaacttcatgggaaatgagtttgggcatcctg 191
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DEVELOPMENTAL STAGE:
mrcsug Type: tuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 4.6%;
Local Similarity 67.2%;
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TISSUE TYPE: tubor
TISSUE TYPE: total tuber
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TOPOLOGY: 11
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                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                          Schnepf, H. Ernest
Knuth, Mark
Pollard, Michael R.
Cardineau, Guy
3: Saliwanchik, Lloyd & Saliwanchik 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                      Narva, Kenneth E.
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(partial) truncated protein; 97,11 % identity
active potato branching enzyme"
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Pred. No. 0.0012;
Pred. No. 38;
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Best Local S
Matches 94
                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLING
APPLICANT: FALKNER, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 352-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2009 ATACGATTATCTTACAAATAATTAAAGATTAAATTATCTTTCGTTTTGTTTTAGATAATT 1950
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
                                                                                                                                  APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                              1829 TGA 1827
                                                                                                                                                                                                                                                                                                                                                                                                                  1889
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                                                                                                                   CORRESPONDENCE ADDRESS:
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Local Similarity 51.4%;
nes 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/633,993 FILING DATE: 19-APR-1996
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                COUNTRY: USA
ZIP: 22313-0299
                                                  STATE:
                                                                 CITY: Alexandria
                                                                                 STREET:
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                                                                                                 ADDRESSEE:
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nucleic acid
DEDNESS: single
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                                                                                 E: Foley & Lardner
1800 Diagonal Road
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                                                                                   Suite 500
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GENERAL INFORMATION:
APPLICANT: POULSEN, PETER
TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
FILE REFERENCE: 674509-2004
CURRENT APPLICATION NUMBER: US/08/981,803
CURRENT FILING DATE: 1997-04-17
EARLIER APPLICATION NUMBER: PCT/EP96/03052
EARLIER FILING DATE: 1996-07-12
                                                                                                                                                            US-08-981-803-29
; Sequence 29, Application US/08981803
; Patent No. 6147279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 ctatcttaaccttcatgggaaatgagtttgggcatccttggtcagtctttacaacattattg 213
                                                                                                                                                                                                                                                                                                                     454 tccctcactagatctttattggccatttatttctt 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 agattttccaagaggcccacaaactcttccaaccggcaaagttctcccctggaaataaca 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 attatgtaatctgttgcttccaaggaggaagttaacttctatttacttggcagaatggat 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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APPLICANT: POULSEN, Peter
TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
FILE REFERENCE: 674509-2003
CURRENT APPLICATION UMBER: US/08/983,440
CURRENT FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 9514437.4
EARLIER APPLICATION NUMBER: PCT/EP96/03053
EARLIER APPLICATION NUMBER: PCT/EP96/03053
EARLIER FILING DATE: 1996-07-12
NUMBER: OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-983-440-29
; Sequence 29, Application US/08983440
; Patent No. 6232122
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                                                                                                                                         US-08-983-440-29
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SEQ ID NO 29
LENGTH: 11478
                                                                   Query Match
Best Local S
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Best Local Similarity 65.1%;
Matches 54; Conservative
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SEQ ID NO 29
LENGTH: 11478
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EARLIER FILING DATE: 1995-07-14
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                       NAME/KEY: variation
LOCATION: (1)..(11478)
OTHER INFORMATION: M stands
                                                                                                                                                                                                                       NAME/KEY: variation LOCATION: (1)..(11478) OTHER INFORMATION: W stands
                                                                                                                                                                                                                                                                                       NAME/KEY: variation LOCATION: (1)...(11478) OTHER INFORMATION: K stands
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: variation
LOCATION: (1)..(11478)
OTHER INFORMATION: B stands
                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(11478)
OTHER INFORMATION: R stands
                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: variation LOCATION: (1)..(114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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107 ttacataaaatgatcaggcttgtcaccatgggtttaggtggtgaaggctatcttaacttc 166
                                                   Match 3.7%;
Local Similarity 65.1%;
nes 54; Conservative
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                                                   Score 36.6; DB Pred. No. 1.2; 0; Mismatches
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Pred. No. 1.2;
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                                                                                     DB 4; Length 11478;
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US-09-351-414-3
                                                                                                                                                                                                               US-08-647-351B-1
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                                                                                                                                                                           Sequence 1, Application US/08647351B Patent No. 5770368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 3
LENGTH: 2088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sheppard, Paul O. APPLICANT: Baildur, Mand APPLICANT: Deisher, Theresa A. APPLICANT: Bishop, Paul D.
                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/351,414
CURRENT FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DISINTEGRIN HOMOLOG FILE REFERENCE: 98-29
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LOCATION: (1)...(2088)
OTHER INFORMATION: n = A,T,C
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LOCATION: (1)...(2088)
OTHER INFORMATION: n is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                            APPLICANT: De Leon, Ricardo
APPLICANT: Rochelle, Paul
TITLE OF INVENTION: Cryptos
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                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          1066 gartaymgngayttyytncarmgnggnggnggngcntgyytnttyaaymgnccnacnaar 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1006 tgyathatggargaracnggngtnwsncaywsnmgnaarttywsnaartgywsnathytn 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 3.6%; Score 36.4; DB 4;
Local Similarity 29.3%; Pred. No. 0.63;
nes 60; Conservative 38; Mismatches 107;
                    STREET:
                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggaggaagttaacttctatttacttggcagaatggatagattttccaagaggcccacaaa 356
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Pasadena
                    225 S. Lake Avenue,
                                        Sheldon & Mak
                                                                              Cryptosporidium Detection 10
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                      9th Floor
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                                                                                                Method
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

OPERATING SYSTEM:

IBM compatible Diskette,

3.50 inch, 1.44 Mb storage

WordPerfect for Windows version 6.1

Windows 95

STATE: 91101

California

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US-09-177-249-5/c
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                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 5801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                      APPLICANT: Goldberg, Robert B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
TITLE OF INVENTION: Development in Plants
FILE REFERENCE: 023070-086120US
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
CURRENT FILING DATE: 1998-10-22
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
                                                                                                                                                                                                                                                                              APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramin
APPLICANT: Margossian, Linda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       APPLICANT:
ORGANISM: Arabidopsis sp
                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: May 9, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Farah, David A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              537 tttgtagacgttaacataagtatgttgttgagagttgttgatcattaaaaatatcatgatt 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3607 base pairs
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55.6%;
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Pred. No.
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; LOCATION: (3872)..(5566)
; OTHER INFORMATION: fertilization-independent endosperm
; OTHER INFORMATION: WD40/polycomb gene genomic sequence
US-09-177-249-5
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Patent No.
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Best Local :
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                                                                                                                                                          APPLICATION NUMBER: JP 05
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05
FILING DATE: 30-SEP-1993
                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NEW POLYPEPTIDE, DNA ENCODING THE TITLE OF INVENTION: POLYPEPTIDE, RECOMBINANT VECTOR BEARING THE DNA AND TITLE OF INVENTION: RECOMBINANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS WELL TITLE OF INVENTION: AS USE THEREOF
                                                                                       FILING DATE: 31-MAR-1994 ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-659-2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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Local Similarity 50.9%;
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CITY: Washington
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 25-SEP-1995
                              NAME: McLeland, Le-Nhung REGISTRATION NUMBER: 31,541 REFERENCE/DOCKET NUMBER: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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Aoyama, Shigemi
Takahashi, Kiyoohito
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Funato, Hirono
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Saeki, Sakiko
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Pred. No. 1.5;
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TELEFAX: 202-8870357 INFORMATION FOR SEQ ID NO:

5

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GENERAL INFORMATION:

APPLICANT: Pauli, Benedicht U.

TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium

TITLE OF INVENTION: Activated Chloride Channel-Adhesion Molecules

FILE REFERENCE: 18617.0052

CURRENT FILING DATE: 1998.11-17

PRIOR APPLICATION NUMBER: US/09/193,562D

CURRENT FILING DATE: 1998.11-17

PRIOR APPLICATION NUMBER: US/60/065,922

PRIOR FILING DATE: 1997-11-17

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 29

LENCTH: 3418

TYPE: DNA

ORGANISM: Homo sapiens

US-09-193-562D-29
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Best Local Similarity 47.7%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                  Query Match 3.4
Best Local Similarity 47.7
Matches 133; Conservative
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LENGTH: 1945 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                             2750 tttttggattagctgtaattttatctatattttatactagaaattatattagaactcaaa 2809
                                                                                                                              2690 ctccacaggaacccagcattcctgatctgggtaccaatatttctgcaatcagtttggcaa 2749
                                                                                                                                                                                                               1613 CATTAAAGCTCAGTAAGTAAATAGTTTTTCAATCTT 1648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1493 TTGAAAAGTGTTCATTAAGTTAATGTATTCTTGCTGGTATTTCTTATTAATCTGATCAGG 1552
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  520 aacattgcttttgtagttttgtagacgttaacataa---gtatgtgttgagagttgttga 576
                                                                     400 atgataaatgccgccgtagattttgatcttgtaagtttttagctgtgctattacattccctc 459
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47.7%; Pred. No. 3.3;
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Pred. No. 1.3;
0; Mismatches 113;
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D48464 RICST4669A
BE414598 SCU011.E0
BE49853 WHE0971_G
AV944141 AV944141
AV921312 AV921312
B1948391 HVSME1000
BG366889 HVSME1000
BE196055 HVSMEh009
                                                                                          AQ690523 nbxb00820
BE427534 PSR7153 I
BE591091 WHE0861_C
BE419958 WWS019, E6
BE517857 WHE0803_A
BE407623 CSB009H05
AV914376 AV914376
BE195228 HYSMEh008
BF065047 HY_CEB002
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	BG521974 Sad72d10 BG551974 Sad72d10 B1465105 Sa107e09 B1699680 Sa125909 BM5956011 S195903.y AM5956011 S195903.y AN751420 ISYS0089 AV442128 AV442128	ത ്ത	. 1 067

ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL SOURCE ORGANISM RESULT 1 AQ690523/c LOCUS VERSION KEYWORDS FEATURES COMMENT DEFINITION ACCESSION source AQ690523 AQ690523.1 GI:5331691 GSS. Clemson University 100 Jordan Hall, Clemson, Tel: 864 656 7288 Fax: 864 656 4293 Unpublished (1998) Contact: Wing RA 1 (bases 1 to 465)
Wing R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome Oryza sativa. Oryza sativa AQ690523

nbxb0082011f CUGI Rice BAC
nbxb0082011f, DNA sequence. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza. Email: rwing@clemson.edu Seq primer: TAATACGACTCACTATAGGG Clemson University Genomics Institute High quality sequence stop: 177. .ass: BAC ends /organism="Oryza sativa"
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/note="Vector: pBeloBAC11; Site_1: HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those Location/Qualifiers . 465 465 SC Library 29634, USA dq DNA linear GSS 01-JUL-1999 Oryza sativa genomic clone

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                                                                                 Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A.,
                                                                                                                                                                                        EST
                                                                                                                                                                                                                                   BE427534 650 bp mRN PSR7153 ITEC PSR Wheat Pericarp/Testa CDNA clone PSR7153, mRNA sequence. BE427534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Organ satisfy Nirocobaro variety.
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                                                                                                                                            P.S., Hsia.C.C., Kang,Y., Lazo,G.R., Miller,R., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed port:
genomes - 20-45 DAP spike cDNA library
                                                                                          Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Triticum.
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International Triticeae EST Cooperative
http://wheat.pw.usda.gov/genome.
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Norfolk, Norwich NR4 7UH UNITED H
Tel: 44 1603 452571 ext. 2587
Fax: 44 1603 502241
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Contact: Bailey P
                                                     West Area, Western Regional Research
800 Buchanan Street, Albany, CA 94710
                                                                                                                          Unpublished (2000)
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Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D.,
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oandersn@pw.usda.gov
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/Glone=lib="ITEC PSR Wheat Pericarp/Testa Library"
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/dev_stage="3:1 mix 10:20 days post anthesis"
/note="Vector: Lambda ZAP II (Stratagene)"
/note="Vector: Lambda ZAP II (Stratagene)"
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/cultivar="Novosibirskaya 67"
/db_xref="taxon:4565"
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                                                                                                                                                   Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Sharifiou, M., Sorrells, M., Warburton, M. and Wenzel, G. International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                 Expressed Sequence Tags Unpublished (2000)
                       Tel: 44 1603 250 260
Fax: 44 1603 250 699
                                                                    Zeneca Wheat Improvement Colney Lane, Norwich NR4
                                                                                                                  Contact:
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wolfgang.schuch@aguk.zeneca.com
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//dev_stage="Adult plant"
//dev_stage="Adult plant"
//lab host="E. coli SOLR"
//note="Vector: Lambda Uni-ZAP XR, excised phagemid;
//note="Vector: Lambda Uni-ZAP XR, excised phagemid;
//site_1: EcoRI; Site_2: xhoI; Plants were grown in the
greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP
were harvested, total RNA and poly(A) RNA were prepared, a
cDNA library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
(Choi, Close, Fenton) at the University of California,
Riverside. Plasmid DNA preparations and DNA sequencing
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/db_xref="taxon:4565"
/clone="WHE0861_C09_F17"
/clone_lib="Wheat 20-45 DAP
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Pred. No. 1.1e-20;
""" matches 3;
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7UH UNITED KINGDOM
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                                                                                                                                                                                                                                                                                                                                                                      Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fento,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rat Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion genomes - Vernalized crown cDNA library
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                                                                                                                                                                          Sequence have been trimmed to remove vector quality sequence with phred score less than. Seq primer: Stratagene SK primer.
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                                                                                                                                                                                                                                                                                                                 Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
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                                                                                                                                                                                                                              Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                    Fax: 5105595818
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/clone_lib="TTEC WWS Wheat Scutellum Library"
/tissue_type="scutellum callus"
/note="M13 Reverse sequencing primer used for clone."
a 70 c 89 g 108 t 1 others
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/dev_stage="Five-week old seedling"
/lab_host="E. coli SOLR"
                                                                    /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0803_A06_B11"
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/cultivar="Novosibirskaya 67"
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R., Miller, R.,
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S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,I.
Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
Sorrells,M., Warburton,M. and Wenzel,G.
International Triticeae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
snermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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                                                                                                                                                                                                                                                                                                                                                                      Tel: 61 62 465496
Fax: 61 62 465000
                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed Sequence Tags for Spunpublished (2000)
Contact: Appels R
Div. of Plant Industry, CSIRO
Camberra ACT 2601 AUSTRALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; Triticeae; Triticum.
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BE402623.1 GI:9362091
                                                                                                                                                                                                                                                                                               http://wheat.pw.usda.gov/genome.
                                                                                                                                                                                                                                                                                                                      International Triticeae EST Cooperative (ITEC)
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                                                                                                                                                                                                                                                                                                                                               rudi@pi.csiro.au
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                                                                                                                                          /organism="Triticum aestivum"
/cultivar="Wyuna"
/db_xref="taxon:4565"
/clone="CSB009H05"
                                             /tissue_type="endosperm"
/dev_stage="8-12 days post anthesis"
/lab_host="Escherichia coli SOLR"
                           /note="Vector:
                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                      /clone_lib="ITEC CSB Wheat Endosperm Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.3%;
97.3%;
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Pred. No. 1.3e-20;
                         Lambda Zap/Bluescript; Site_1:
  Plants grown
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XhoI;
18C/13C
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TITLE
JOURNAL
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Best Local (
                                                                                                                           Matches
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Best Local Similarity
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                               102
160
                                                              100
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              tagcattacataaaatgatcaggcttgtcaccatgggtttaggtggtgatggctatctta 161
                                                                             aggatatgtatgatttcatggctctggatag-gcttcaactcttcgcattgatcgtggca 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aggatatgtatgatttcatggctctggatag-gcttcaactcttcgcattgatcgtggca 101
TAGCATTACATAAAATGATCAGGCTTGTCACCATGGGTTTAGGTGGCGAAGGCTATCTTA
                                                              AGGATATGTATGATTCATGGCTCTGGATAGACCTTCAACCCCTCGCATTGATCGTGGCA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGCATTACATAAAATGATCAGGCTTGTCACCATGGGTTTAGGTGGCGAAGGCTATCTTA
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                                                                                                                             144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV914376 K. Sato unpublished cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barley EST sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sato, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV914376.1
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81-559-81-6856
81-559-81-6855
                                                                                                                             Conservative
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                                                                                                                                                                                                                      /organism="Hordeum vulgare subsp.
/cultivar="Haruna Nijo"
/db_xref="taxon:112509"
/clone="bbgx55011"
/clone_lib="K. Sato unpublished cl
Nijo germination shoots"
/tissue_type="shoots"
/dev_stage="germination"
/dev_stage="116 g 135 t ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saisho, D.
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used. 1.0 Kbp average insert size."
a 116 c 144 g 167 t 1 others
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97.3%;
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Pred. No. 1.3e-20;
                                                                                                                                        Score 130; DB 9;
Pred. No. 6.9e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu, Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rwing@clemson.edu
Total hq bases = 408
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
On Jun 26, 2000 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 864 656 7288 Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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Location/Qualifiers
                                                                                                                                                                                                       /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, S) Close, TJ Close). Whole spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
this clone see http://www.genome.clemson.edu/orders Also
see close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
                                                                                                                                                                                    above. For more details on library preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Hordeum vulgare 5-45 HVcDNA0009 (5 to 45 DAP)"
                                                                                                                                                       sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="Morex"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="HVSMEh0089P20f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Hordeum vulgare"
                                                                                                                          /www.genome.clemson.edu/projects/barley.
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HV_CEb0022L05f Hordeum vulgare seedling green leaf EST libra
HVcDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University
100 Jordan Hall, Clemson,
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wing R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
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BF065047
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leaf cDNA library
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/tissue_type="seedling green leaf"
/lab_host="SOLR"
/lab_host="SOLR"
/lab_host="SOLR"
/note="Wector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
/note="Wector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
/note="Wector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
/note="Wector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
/note="Wector: lambdaZAP; Site_1: EcoR1; January In the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate 5874 (AvrMla6
) of Blumeria graminis f. sp. hordei, and leaves were
harvested 20 and 24 hr post-inoculation and snap frozen;
uninoculated leaves were harvested 20 hr post-inoculation
(Wei, Wise). In the TJ Close lab at the University of
California, Riverside, total RNA was prepared from each
sample pool, equal quantities of all three RNA pools were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rwing@clemson.edu
                                                                                                                                                                                                                                                                                                /clone="HV_CEb0022L05f"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HVcDNA0005 (Blumeria challenged)"
                                                                                                                                                                                                                                                                                                                                                                  /organism="Hordeum vulgare"
/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
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Pred. No. 7.6e-20;
Pred. No. 7.6e-20;
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seedling green leaf EST library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RICS14669A Rice green s
D48464
D48464.1 GI:702173
EST.
Oryza sativa.
                                                                                                                                                                                                                                                                                                    National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                            Sasaki,T., Miyao,A. and Yan
Rice cDNA from callus 1995
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 448)
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                                                                                                                                                                                                                                                                                     305-8602,
                                                                                                                                                                                                                                                                                                                                                           Contact: Takuji Sasaki
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                        131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at the Clemson University Genomics Institute (CUGI) [Regum Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/projects/barley also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/gspages/bgn/31/cover.html)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                  tsasaki@abr.affrc.go.jp,
Location/Qualifiers
            /organism="Oryza sativa"
/strain="Nipponbare"
/db_xref="taxon:4530"
/clone_lib="Rice green shoot"
/note="Green shoot (8 days old)"
a 81 c 113 g 122 t 1
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96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  shoot Oryza sativa cDNA,
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Pred. No. 7.7e-20;
D; Mismatches 5;
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                                                                                                                                                                                                             URL: http://rgp.dna.affrc.go.jp/
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                   1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acttcatgggaaatgagtttgggcatcctg 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tagcattacataaaatgatcaggcttgtcaccatgggtttaggttggtggaggctatctta 161
CTTGTCACCATGGGTTTAGGTGGTGAAGGCTATCTTAACTTCATGGGAAATGAGTTTGGG
                                                                    TCGGCACGAGCTTCAACTCCTCGCATTGATCGTGGCATAGCATTACATAAAATGATCAGG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTTCATGGGAAATGAGTTTGGGCATCCTG 194
                                                                                                                                       121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson, O. A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Lazo, G. R., Lin, J. J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G. International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tays for Species of the Triticeae Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE414598 743 bp mRNA linear EST 24-JUL-2000 SCU011.E01.R990714 ITEC SCU Wheat Endosperm Library Triticum aestivum cDNA clone SCU011.E01, mRNA sequence.
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Spermatophyta; Magnoliophyta; Liliopsida;
Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                               http://wheat.pw.usda.gov/genome
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 61 2 6620 3409 Fax: 61 2 6622 2080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Centre for Plant Conservation Genetics, PO Box 157, Lismore NSW 2480 AUSTRALIA
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BE414598
                                                                                                                                                                                                                                                                                                                                                                                                                                   International Triticeae EST Cooperative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: tholton@scu.edu.au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Holton
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                                                                                                                                                                                                                                        /tissue_type="endosperm"
/note="Vector: Bluescript
    159 c    178 g    190
                                                                                                                                                                                                                                                                                            /clone="SCU011.E01"
/clone_lib="ITEC_SCU Wheat Endosperm Library"
                                                                                                                                                                                                                                                                                                                                               /organism="Triticum aestivum"
/cultivar="Wyuna"
                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4565"
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                                                                                                                                                     11.7%;
95.3%;
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91.3%;
                                                                                                                                 Score 117.4; DB 10;
Pred. No. 6.2e-17; '
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a; Poales; Poaceae; Pooideae
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Best Local (
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                                                                                                                                                     883 gtttatgacatctgagcaccagtatgtttcacggaaacatgaggaagataaggtgatcat 942
                                                                          943 cctcaaaagaggagatttggtatttgttttcaacttccacttggagcaatagcttttttg 1001
                                                        145 CTTCGAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234
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                                                                                                                                 85 GTTTATGACATCTGAGCACCAGTATGTTTCACGGAAACACGAGGAAGATAAGGTGATCAT 144
                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacif. West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fay: Finesers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE498533 494 bp mRNA linear EST 04-AUG-2000 WHE0971_G03_M05ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE0971_G03_M05, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence with phred score less Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticeum.
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                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                     /clone_lib="wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Site_2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0971_G03_M05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Triticum aestivum"
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                                                                                                                                                                                                                              11.4%;
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Pred. No. 3.2e-16;
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AUTHORS
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AV921312/c
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Best Local (
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Local Similarity
nes 116; Conserv
                                      Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
                                                                                                                                                                                                                                                                                                   AV921312 692 bp mRNA
AV921312 K. Sato unpublished cONA library,
germination shoots Hordeum vulgare subsp. v
bags23a09 3', mRNA sequence.
AV921312
AV921312.1 GI:18217091
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AV944141
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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AV944141.1 GI:18239938
EST
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 4
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Location/Qualifiers
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Fax: 81-559-81-6855
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/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/dev_stage="adult, heading stage"
180 c 145 g 177 t 2 oth
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/clone="bah20e24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="H602".
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Pred. No. 3.4e-16;
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// cv. Haruna |
// vulgare cDNA
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                                                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University
                                                                                                                                                                                                                                                                                                                                                                               for barley genomics: Fusarium infected Morex spike cDNA library
Unpublished (2001)
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wing,R., Muehlbauer,G.J., Close,T.J., Kleinhofs,A., Wise,R., Heinen,S., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Fenton,R.D., Malatrasi,M., Choi,D.W., Oates,R. and Main
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI948391 728 bp mRNA linear EST 19-OCT-2001
HVSME10009F19f Hordeum vulgare spike EST library HVcDNA0012
(Fusarium infected) Hordeum vulgare cDNA clone HVSME10009F19f, mRNA
                                                                                                                                                                                                         Seq primer: AATTAACCCTCACTAAAGGG High quality sequence stop: 680.
                                                                                                                                                                                                                                                Email: rwing@clemson.edu
Total hq bases = 639
                                                                                                                                                                                                                                                                                       Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                       Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI948391.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                            100 Jordan Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ò.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="K. Sato unpublished cDNA library, cv. Haruna
Nijo germination shoots"
/tissue_type="shoots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Hordeum vulgare subsp. vulgare"
Cultivar="Haruna Nijo"
/db_xref="taxon:112509"
/clone="bags23a09"
/note="Vector:
                 /tissue_type="Spike"
/lab_host="TJC121"
                                                        /clone_lib="Hordeum vulgare spike EST library HVcDNA0012
(Fusarium infected)"
                                                                                                                 /cultivar="Morex"
/db_xref="taxon:4513"
                                                                                                                                                  /organism="Hordeum vulgare"
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184 c 147 g 176 t
                                                                                             clone="HVSME10009F19f"
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Pred. No. 3.4e-16;
pBluescript SK(-); Site_1: EcoRI; Site_2:
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ORIGIN BASE COUNT

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Query Match
Best Local Similarity
Matches 116; Conserv
                                    943 cctcaaaagaggagatttggtatttgttttcaacttccactggagcaatagcttttttg 1001
                                                                                                                                                                      883 gtttatgacatctgagcaccagtatgtttcacggaaacatgaggaagataaggtgatcat 942
122 CTTCGAAAGAGGAGATTTGGTATTTGTTTTCAACTTCCACTGGAGCAATAGCTTTTTTG
                                                                                                                                      62 GTTTATGACATCTGAGCACCAGTATGTTTCTCGGAAACATGAGGAAGATAAGGTGATCAT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 a
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepared from each sample pool, equal quantitles of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically ancies EST rescues for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
151 c 188 g 192 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.genome.clemson.edu/projects/barley. To order
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               above. For more details on library preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XhoI; Plants were grown at the University of Minnesota in the GJ Muehlbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TJ Close lab at the University of California, Riverside, total RNA was the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          this clone see http://www.genome.clemson.edu/orders Also
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                                                                                                                                                                                                                                                                                                         11.4%;
97.5%;
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                                                                                                                                                                                                                                                                     Score 114.2; DB 10; Pred. No. 3.4e-16; 0; Mismatches 3;
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180
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